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26119 7590 08/24/2010

KLARQUIST SPARKMAN LLP
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PORTLAND, OR 97204

EXAMINER	
RIGGS II, LARRY D	
ART UNIT	PAPER NUMBER
1631	

DATE MAILED: 08/24/2010

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/800,340	03/12/2004	Lee Weng	3382-83763-01	9918

TITLE OF INVENTION: METHODS OF ANALYZING MULTI-CHANNEL PROFILES

APPLN. TYPE	SMALL ENTITY	ISSUE FEE DUE	PUBLICATION FEE DUE	PREV. PAID ISSUE FEE	TOTAL FEE(S) DUE	DATE DUE
nonprovisional	NO	$1510	$300	$0	$1810	11/24/2010

THE APPLICATION IDENTIFIED ABOVE HAS BEEN EXAMINED AND IS ALLOWED FOR ISSUANCE AS A PATENT. PROSECUTION ON THE MERITS IS CLOSED. THIS NOTICE OF ALLOWANCE IS NOT A GRANT OF PATENT RIGHTS. THIS APPLICATION IS SUBJECT TO WITHDRAWAL FROM ISSUE AT THE INITIATIVE OF THE OFFICE OR UPON PETITION BY THE APPLICANT. SEE 37 CFR 1.313 AND MPEP 1308.

THE ISSUE FEE AND PUBLICATION FEE (IF REQUIRED) MUST BE PAID WITHIN THREE MONTHS FROM THE MAILING DATE OF THIS NOTICE OR THIS APPLICATION SHALL BE REGARDED AS ABANDONED. THIS STATUTORY PERIOD CANNOT BE EXTENDED. SEE 35 U.S.C. 151. THE ISSUE FEE DUE INDICATED ABOVE DOES NOT REFLECT A CREDIT FOR ANY PREVIOUSLY PAID ISSUE FEE IN THIS APPLICATION. IF AN ISSUE FEE HAS PREVIOUSLY BEEN PAID IN THIS APPLICATION (AS SHOWN ABOVE), THE RETURN OF PART B OF THIS FORM WILL BE CONSIDERED A REQUEST TO REAPPLY THE PREVIOUSLY PAID ISSUE FEE TOWARD THE ISSUE FEE NOW DUE.

HOW TO REPLY TO THIS NOTICE:

I. Review the SMALL ENTITY status shown above.

If the SMALL ENTITY is shown as YES, verify your current SMALL ENTITY status:

A. If the status is the same, pay the TOTAL FEE(S) DUE shown above.

B. If the status above is to be removed, check box 5b on Part B - Fee(s) Transmittal and pay the PUBLICATION FEE (if required) and twice the amount of the ISSUE FEE shown above, or

If the SMALL ENTITY is shown as NO:

A. Pay TOTAL FEE(S) DUE shown above, or

B. If applicant claimed SMALL ENTITY status before, or is now claiming SMALL ENTITY status, check box 5a on Part B - Fee(s) Transmittal and pay the PUBLICATION FEE (if required) and 1/2 the ISSUE FEE shown above.

II. PART B - FEE(S) TRANSMITTAL, or its equivalent, must be completed and returned to the United States Patent and Trademark Office (USPTO) with your ISSUE FEE and PUBLICATION FEE (if required). If you are charging the fee(s) to your deposit account, section "4b" of Part B - Fee(s) Transmittal should be completed and an extra copy of the form should be submitted. If an equivalent of Part B is filed, a request to reapply a previously paid issue fee must be clearly made, and delays in processing may occur due to the difficulty in recognizing the paper as an equivalent of Part B.

III. All communications regarding this application must give the application number. Please direct all communications prior to issuance to Mail Stop ISSUE FEE unless advised to the contrary.

IMPORTANT REMINDER: Utility patents issuing on applications filed on or after Dec. 12, 1980 may require payment of maintenance fees. It is patentee's responsibility to ensure timely payment of maintenance fees when due.

PTOL-85 (Rev. 08/07) Approved for use through 08/31/2010.

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INSTRUCTIONS: This form should be used for transmitting the ISSUE FEE and PUBLICATION FEE (if required). Blocks 1 through 5 should be completed where appropriate. All further correspondence including the Patent, advance orders and notification of maintenance fees will be mailed to the current correspondence address as indicated unless corrected below or directed otherwise in Block 1, by (a) specifying a new correspondence address; and/or (b) indicating a separate "FEE ADDRESS" for maintenance fee notifications.

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(Depositor's name)
(Signature)
(Date)

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nonprovisional	NO	$1510	$300	$0	$1810	11/24/2010

EXAMINER	ART UNIT	CLASS-SUBCLASS
RIGGS II, LARRY D	1631	702-019000

1. Change of correspondence address or indication of "Fee Address" (37 CFR 1.363).

❑ Change of correspondence address (or Change of Correspondence Address form PTO/SB/122) attached.

❑ "Fee Address" indication (or "Fee Address" Indication form PTO/SB/47; Rev 03-02 or more recent) attached. **Use of a Customer Number is required.**

2. For printing on the patent front page, list

(1) the names of up to 3 registered patent attorneys or agents OR, alternatively,

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1 _____

2 _____

3 _____

3. ASSIGNEE NAME AND RESIDENCE DATA TO BE PRINTED ON THE PATENT (print or type)

PLEASE NOTE: Unless an assignee is identified below, no assignee data will appear on the patent. If an assignee is identified below, the document has been filed for recordation as set forth in 37 CFR 3.11. Completion of this form is NOT a substitute for filing an assignment.

(A) NAME OF ASSIGNEE (B) RESIDENCE: (CITY and STATE OR COUNTRY)

Please check the appropriate assignee category or categories (will not be printed on the patent) : ❑ Individual ❑ Corporation or other private group entity ❑ Government

4a. The following fee(s) are submitted:

❑ Issue Fee

❑ Publication Fee (No small entity discount permitted)

❑ Advance Order - # of Copies _____

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❑ A check is enclosed.

❑ Payment by credit card. Form PTO-2038 is attached.

❑ The Director is hereby authorized to charge the required fee(s), any deficiency, or credit any overpayment, to Deposit Account Number _____ (enclose an extra copy of this form).

5. **Change in Entity Status** (from status indicated above)

❑ a. Applicant claims SMALL ENTITY status. See 37 CFR 1.27.

❑ b. Applicant is no longer claiming SMALL ENTITY status. See 37 CFR 1.27(g)(2).

NOTE: The Issue Fee and Publication Fee (if required) will not be accepted from anyone other than the applicant; a registered attorney or agent; or the assignee or other party in interest as shown by the records of the United States Patent and Trademark Office.

Authorized Signature _____ Date _____

Typed or printed name _____ Registration No. _____

This collection of information is required by 37 CFR 1.311. The information is required to obtain or retain a benefit by the public which is to file (and by the USPTO to process) an application. Confidentiality is governed by 35 U.S.C. 122 and 37 CFR 1.14. This collection is estimated to take 12 minutes to complete, including gathering, preparing, and submitting the completed application form to the USPTO. Time will vary depending upon the individual case. Any comments on the amount of time you require to complete this form and/or suggestions for reducing this burden, should be sent to the Chief Information Officer, U.S. Patent and Trademark Office, U.S. Department of Commerce, P.O. Box 1450, Alexandria, Virginia 22313-1450. DO NOT SEND FEES OR COMPLETED FORMS TO THIS ADDRESS. SEND TO: Commissioner for Patents, P.O. Box 1450, Alexandria, Virginia 22313-1450.

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Determination of Patent Term Adjustment under 35 U.S.C. 154 (b)
(application filed on or after May 29, 2000)

The Patent Term Adjustment to date is 378 day(s). If the issue fee is paid on the date that is three months after the mailing date of this notice and the patent issues on the Tuesday before the date that is 28 weeks (six and a half months) after the mailing date of this notice, the Patent Term Adjustment will be 378 day(s).

If a Continued Prosecution Application (CPA) was filed in the above-identified application, the filing date that determines Patent Term Adjustment is the filing date of the most recent CPA.

Applicant will be able to obtain more detailed information by accessing the Patent Application Information Retrieval (PAIR) WEB site (http://pair.uspto.gov).

Any questions regarding the Patent Term Extension or Adjustment determination should be directed to the Office of Patent Legal Administration at (571)-272-7702. Questions relating to issue and publication fee payments should be directed to the Customer Service Center of the Office of Patent Publication at 1-(888)-786-0101 or (571)-272-4200.

PTOL-85 (Rev. 08/07) Approved for use through 08/31/2010.

Notice of Allowability	Application No.	Applicant(s)	
	10/800,340	WENG, LEE	
	Examiner	Art Unit	
	LARRY D. RIGGS II	1631	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address--

All claims being allowable, PROSECUTION ON THE MERITS IS (OR REMAINS) CLOSED in this application. If not included herewith (or previously mailed), a Notice of Allowance (PTOL-85) or other appropriate communication will be mailed in due course. **THIS NOTICE OF ALLOWABILITY IS NOT A GRANT OF PATENT RIGHTS.** This application is subject to withdrawal from issue at the initiative of the Office or upon petition by the applicant. See 37 CFR 1.313 and MPEP 1308.

1. ☒ This communication is responsive to *amendments and arguments discussed in the telephonic interview 6/8/2010*.

2. ☒ The allowed claim(s) is/are *1-18, 20-30, 32-36, 38-57, 66, 67, 70-105, 107-164 and 166-188*.

3. ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
   a) ☐ All b) ☐ Some* c) ☐ None of the:
      1. ☐ Certified copies of the priority documents have been received.
      2. ☐ Certified copies of the priority documents have been received in Application No. _____ .
      3. ☐ Copies of the certified copies of the priority documents have been received in this national stage application from the International Bureau (PCT Rule 17.2(a)).

   * Certified copies not received: _____.

Applicant has THREE MONTHS FROM THE "MAILING DATE" of this communication to file a reply complying with the requirements noted below. Failure to timely comply will result in ABANDONMENT of this application.
THIS THREE-MONTH PERIOD IS NOT EXTENDABLE.

4. ☐ A SUBSTITUTE OATH OR DECLARATION must be submitted. Note the attached EXAMINER'S AMENDMENT or NOTICE OF INFORMAL PATENT APPLICATION (PTO-152) which gives reason(s) why the oath or declaration is deficient.

5. ☐ CORRECTED DRAWINGS (as "replacement sheets") must be submitted.
   (a) ☐ including changes required by the Notice of Draftsperson's Patent Drawing Review (PTO-948) attached
      1) ☐ hereto or 2) ☐ to Paper No./Mail Date _____.
   (b) ☐ including changes required by the attached Examiner's Amendment / Comment or in the Office action of Paper No./Mail Date _____.

   Identifying indicia such as the application number (see 37 CFR 1.84(c)) should be written on the drawings in the front (not the back) of each sheet. Replacement sheet(s) should be labeled as such in the header according to 37 CFR 1.121(d).

6. ☐ DEPOSIT OF and/or INFORMATION about the deposit of BIOLOGICAL MATERIAL must be submitted. Note the attached Examiner's comment regarding REQUIREMENT FOR THE DEPOSIT OF BIOLOGICAL MATERIAL.

Attachment(s)

1. ☐ Notice of References Cited (PTO-892)
2. ☐ Notice of Draftperson's Patent Drawing Review (PTO-948)
3. ☒ Information Disclosure Statements (PTO/SB/08), Paper No./Mail Date 3/19/2010
4. ☐ Examiner's Comment Regarding Requirement for Deposit of Biological Material
5. ☐ Notice of Informal Patent Application
6. ☐ Interview Summary (PTO-413), Paper No./Mail Date _____ .
7. ☒ Examiner's Amendment/Comment
8. ☒ Examiner's Statement of Reasons for Allowance
9. ☐ Other _____.

EXAMINER'S AMENDMENT

An examiner's amendment to the record appears below. Should the changes and/or additions be unacceptable to applicant, an amendment may be filed as provided by 37 CFR 1.312. To ensure consideration of such an amendment, it MUST be submitted no later than the payment of the issue fee.

Authorization for this examiner's amendment was given in a telephone interview with attorney Gregory Maurer on 8/10/2010.

The application has been amended as follows:

Listing of Claims

1. **(Currently Amended)** A method for generating at least one error-corrected experiment profile of at least one experiment profile in a plurality of pairs of profiles $\{A_m, C_m\}$, where $m = 1, 2, \ldots, M$, and M is the number of the pairs of profiles; and wherein, for each $m \in \{1, 2, \ldots, M\}$, A_m is an experiment profile, and C_m is a reference profile; and wherein $\{A_m\}$ represents experiment profiles in said plurality of pairs of profiles $\{A_m, C_m\}$ and $\{C_m\}$ represents reference profiles in said plurality of pairs of profiles $\{A_m, C_m\}$, said method comprising:

(a) calculating, on a suitably programmed computer, an average reference profile $\bar{C}$ of said plurality of reference profiles $\{C_m\}$ where $m = 1, 2, \ldots, M$;

(b) determining, on a suitably programmed computer, for at least one profile pair $\{A_m, C_m\}$where $m \in \{1, 2, \ldots, M\}$ of said plurality of pairs of profiles $\{A_m, C_m\}$ a differential reference profile, $\underline{\bar{C}_{diff}(m,k)}$, computed between C_m and $\bar{C}$, **wherein said average reference profile $\bar{C}$ comprises data set $\{\bar{C}(k)\}$**;

(c) via said differential reference profile determined for said profile pair, removing, on a suitably programmed computer, systematic cross-experiment error from an experiment profile A_m of said at least one profile pair $\{A_m, C_m\}$ where $m \in \{1, 2, \ldots, M\}$ to generate a first error-corrected experiment profile A'_m for each $m \in \{1, 2, \ldots, M\}$, wherein said experiment profile A_m comprises a first data set, $\{A_m(k)\}$, said reference profile C_m comprises a second data set, ~~said average reference profile $\bar{C}$ comprises data set $\{\bar{C}(k)\}$~~, and said first error-corrected experiment profile A'_m comprises data set

$\{A'_m(k)\}$; wherein said first data set comprises measurements, ~~error-model-based transformed measurements, or logarithm-based transformed measurements~~ of a plurality of different cellular constituents measured in a sample having been subject to a first condition, said second data set comprises measurements, ~~error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents measured in a sample having been subject to a second condition; and wherein k = 1, 2, ..., N; k is an index of measurements, ~~error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents, N being the total number of measurements, ~~error-model-based transformed measurements, or logarithm-based transformed measurements,~~ wherein generating respective $A'_m(k)$ of said first error-corrected experiment profile A'_m comprises subtracting $C_{diff}(m,k)$ from $A_m(k)$; and

~~(d) obtaining a data set $\{A''_m(k)\}$, wherein obtaining said data set $\{A''_m(k)\}$ comprises combining said first error-corrected experiment profile A'_m with said experiment profile A_m using a weighing factor $\{w(k), k = 1, 2, ..., N$, wherein $w(k)$ is a weighing factor for the k'th measurement; and~~

~~(e)~~ (d) outputting to a user, a user interface device, a computer readable storage medium, or a local or remote computer system; or displaying: said first error-corrected experiment profile $A'_m[[,]]$ or said data set $\{A'_m(k)\}$ ~~, a second error-corrected experiment profile A''_m, or said data set $\{A''_m(k)\}$, wherein said second error-corrected experiment profile A''_m comprises said data set $\{A''_m(k)\}$~~.

2. (Previously Presented) The method of claim 1, wherein said steps (b) and (c) are performed for each profile pair $\{A_m, C_m\}$ where $m \in \{1, 2, \ldots, M\}$.

3. **(Currently Amended)** The method of claim 2, wherein each of said experiment profile A_m and said reference profile C_m comprises measurements~~, error-model-based transformed measurements, or logarithm based transformed measurements~~ of said plurality of different cellular constituents from the same experimental reaction.

4. (Previously Presented) The method of claim 3, wherein said $\bar{C}(k)$ is calculated according to the equation

$$\bar{C}(k) = \frac{1}{M}\sum_{m=1}^{M} C_m(k)$$

wherein said differential reference profile is determined according to the equation

$$C_{diff}(m,k) = C_m(k) - \bar{C}(k)$$

and wherein said first error-corrected experiment profile A'_m is generated according to the equation

$$A'_m(k) = A_m(k) - C_{diff}(m,k)$$

wherein $\{A_m(k)\}$ is said first data set of experiment profile A_m.

5. **(Currently Amended)** The method of claim 4, further comprising:

~~(d)~~ (e) calculating, for one or more remaining profile pairs out of said profile pairs $\{A_m, C_m\}$, a respective second error-corrected experiment profile A''_m; and

~~(e)~~ (f) outputting to, a user interface device, a computer readable storage medium, or a local or remote computer system; or displaying; said respective second error-corrected experiment profile A''_m or ~~said~~ a data set $\{A''_m(k)\}$.

6. **(Previously Presented)** The method of claim 5, wherein said second error-corrected experiment profile A''_m is calculated according to the equation

$$A''_m(k) = (1-w(k)) \cdot A_m(k) + w(k) \cdot A'_m(k).$$

7. **(Currently Amended)** The method of claim 6, further comprising determining ~~said~~ a weighing factor $w(k)$ according to the equation

$$w(k) = 1 - e^{-a \cdot \left[\frac{\sum_{m=1}^{M} bkgstd(m,k)}{avg\_bkgstd}\right]^2}$$

where avg_bkgstd is an average background standard error.

8. **(Previously Presented)** The method of claim 7, further comprising determining said avg_bkgstd according to the equation

$$avg\_bkgstd = \frac{1}{N} \sum_{k=1}^{N} \left[\frac{1}{M} \sum_{m=1}^{M} bkgstd(m,k)\right]$$

where *bkgstd (m, k)* is background standard error of $C_m(k)$.

9. (Previously Presented) The method of claim 4, further comprising determining errors $\{\sigma'_m(k)\}$ of said data set $\{A'_m(k)\}$ in said first error-corrected experiment profile A'_m.

10. (Previously Presented) The method of claim 9, further comprising determining said errors $\{\sigma'_m(k)\}$ according to the equation

$$\sigma'_m(k) = \sqrt{\sigma_m^2(k) + mixed\_\sigma_m^2(k) - 2 \cdot Cor(k) \cdot \sigma_m(k) \cdot mixed\_\sigma_m(k)}$$

where $\sigma_m(k)$ is the standard error of $A_m(k)$, the method further comprising determining $mixed\_\sigma_m(k)$ according to the equation

$$mixed\_\sigma_m(k) = \frac{\sigma_m(k) + (M-1)\sigma_{ref}(k)}{M}$$

where $\sigma_{ref}(k) = \sqrt{\frac{1}{M-1}\sum_{m}^{M}(C_m(k) - \bar{C}(k))^2}$

and where Cor(k) is a correlation coefficient between said experiment profile A_m and said reference profile C_m.

11. (Previously Presented) The method of claim 10, further comprising determining said Cor(k) according to the equation

$$Cor(k) = CorMax \cdot \left[1 - e^{-0.5 \cdot \left[\frac{\bar{C}(k)}{mixed\_bkgstd}\right]^2}\right]$$

where CorMax is a number between 0 and 1.

12. (Previously Presented) The method of claim 7, further comprising determining errors $\{\sigma''_m(k)\}$ of said data set $\{A''_m(k)\}$ in said second error-corrected experiment profile A''_m.

13. (Previously Presented) The method of claim 12, wherein said errors $\{\sigma''_m(k)\}$ are determined according to the equation

$$\sigma''_m(k) = \sqrt{[1 - w(k)] \cdot \sigma_m^2(k) + w(k)\sigma'^2_m(k)}$$

where $\sigma_m(k)$ is the standard error of $A_m(k)$, the method further comprising (i) determining $\sigma'_m(k)$ according to the equation

$$\sigma'_m(k) = \sqrt{\sigma_m^2(k) + mixed\_\sigma_m^2(k) - 2 \cdot Cor(k) \cdot \sigma_m(k) \cdot mixed\_\sigma_m(k)}, \text{ and}$$

(ii) determining $mixed\_\sigma_m(k)$ according to the equation

$$mixed\_\sigma_m(k) = \frac{\sigma_m(k) + (M-1) \cdot \sigma_{rel}(k)}{M}$$

where $\sigma_{rel}(k) = \sqrt{\frac{1}{M-1}\sum_m^M (e_m(k) - \bar{C}(k))^2}$

and where Cor(k) is a correlation coefficient between said experiment profile A_m and said reference profile C_m.

14. (Previously Presented) The method of claim 13, further comprising determining said Cor(k) according to the equation

$$Cor(k) = CorMax \cdot \left[1 - e^{-a.s.\left[\frac{\bar{S}(k)}{avg\_sigma}\right]^2}\right]$$

where CorMax is a number between 0 and 1.

15. (Previously Presented) The method of claim 2, wherein said experiment profile A_m and said reference profile C_m of each said profile pair $\{A_m, C_m\}$ are measured in a two-channel microarray experiment.

16. (Previously Presented) The method of claim 15, wherein said reference profiles $\{C_m\}$, where $m = 1, 2, \ldots, M$, are measured with samples labeled with a same label.

17. (Previously Presented) The method of claim 2, wherein at least one of said plurality of pairs of profiles $\{A_m, C_m\}$ is a virtual profile.

18. **(Currently Amended)** The method of claim 1, wherein said plurality of pairs of profiles $\{A_m, C_m\}$ are ~~transformed profiles each comprising error model-based transformed measurements, or logarithm-based~~ transformed measurements of said plurality of different cellular constituents in data set $\{A_m(k)\}$ and data set $\{C_m(k)\}$, respectively; and wherein said data set $\{A_m(k)\}$ is said first data set, and

said data set $\{C_m(k)\}$ is said second data set.

19. (Cancelled)

20. **(Currently Amended)** The method of claim 1, further comprising:

(a0) removing nonlinearity, prior to said calculating step (a), from measurements~~, error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents to generate said plurality of pairs of profiles $\{A_m, C_m\}$ comprising said experiment profile A_m and reference profile C_m.

21. **(Currently Amended)** The method of claim 20, wherein said removing step (a0) comprises:

(a01) calculating an average profile of pre-experiment profiles $\{A_m^{pre}\}$ and pre- reference profiles $\{C_m^{pre}\}$; wherein each of said pre-experiment profiles comprises measurements~~, error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents measured in said sample having been subject to said first condition, which when nonlinearity is removed therefrom, produces each said experiment profile A_m; and wherein each of said pre-reference profiles comprises measurements~~, error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents measured in said

sample having been subject to said second condition, which when nonlinearity is removed therefrom, produces each said reference profile C_m; and

(a0ii) calculating first differences between each of said pre-experiment profiles $\{A_m^{pre}\}$ and said average profile; calculating second differences between each of said pre-reference profiles $\{C_m^{pre}\}$ and said average profile; adjusting, wherein the adjusting comprises correcting nonlinearity, each of said pre-experiment profiles $\{A_m^{pre}\}$ based on said first differences between each of said pre-experiment profiles $\{A_m^{pre}\}$ and said average profile, thereby generating each said experiment profile A_m; and adjusting, wherein the adjusting comprises correcting nonlinearity, each of pre-reference profiles $\{C_m^{pre}\}$ based on said second differences between each of said pre-reference profiles $\{C_m^{pre}\}$ and said average profile, thereby generating each said reference profile C_m.

22. **(Currently Amended)** The method of claim 21, further comprising calculating said first differences based on a first subset of said measurements~~, error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents in said pre-experiment profiles $\{A_m^{pre}\}$ and said average profile; and calculating said second differences based on a second subset of said measurements~~, error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said

plurality of different cellular constituents in said pre-reference profiles $\{C_m^{pre}\}$ and said average profile.

23. **(Currently Amended)** The method of claim 22, wherein said first subset consists of measurements~~, error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents that are ranked similarly between each of said pre-experiment profiles $\{A_m^{pre}\}$ and said average profile, and said second subset consists of measurements~~, error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents that are ranked similarly between each of said pre-reference profiles $\{C_m^{pre}\}$ and said average profile.

24. **(Currently Amended)** The method of claim 23, wherein said adjusting step (a0ii) is carried out by a method comprising:

(ii1) binning said first subset into a first plurality of bins, wherein each of said first plurality of bins consists of measurements~~, error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents in one of said pre-experiment profiles $\{A_m^{pre}\}$ and said average profile having a value in a given range; and binning said second subset into a second plurality of bins, wherein each of said second plurality of bins consists

of measurements, ~~error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents in one of said pre-reference profiles $\{C_m^{pre}\}$ and said average profile having a value in a given range;

(ii2) calculating, in each bin of said first plurality of bins, a first mean difference between a feature value of measurements, ~~error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said one of said pre-experiment profiles $\{A_m^{pre}\}$ and a feature value of said average profile, and calculating a second mean difference between a feature value of measurements, ~~error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said one of said pre-reference profiles $\{C_m^{pre}\}$ and a feature value of said average profile;

(ii3) determining a first curve of said first mean difference as a first function of values of measurements, ~~error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents for said one of said pre-experiment profiles $\{A_m^{pre}\}$, wherein said first function is represented by, $nonlinear\_A_m^{pre}$; and determining a second curve of said second mean difference as a second function of values of measurements, ~~error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents for said one of said

pre-reference profiles $\{C_m^{pre}\}$, wherein said second function is represented by $nonlinear\_C_m^{pre}$; and

(ii4) adjusting each of said pre-experiment profiles $\{A_m^{pre}\}$ according to the equation:

$$A_m(k) = A_m^{pre}(k) - nonlinear\_A_m^{pre}(k),$$

and adjusting each of said pre-reference profiles $\{C_m^{pre}\}$ according to the equation:

$$C_m(k) = C_m^{pre}(k) - nonlinear\_C_m^{pre}(k),$$

where k = 1, ... , N; and where $A_m^{pre}(k)$ and $C_m^{pre}(k)$ are data sets of each of said pre-experiment profiles $\{A_m^{pre}\}$ and each of said pre-reference profiles $\{C_m^{pre}\}$, respectively; and where $A_m(k)$ and $C_m(k)$ are said first data set and said second data set, respectively.

25. **(Currently Amended)** The method of claim 1, further comprising:

(a0) normalizing, prior to said calculating step (a), measurements~~, error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents in a pre-experiment profile A_m^{pre} and a pre-reference profile C_m^{pre} to generate said experiment profile A_m and said reference profile C_m, respectively.

26. (**Currently Amended**) The method of claim 25, wherein said normalizing step (a0) comprises normalizing a data set $A_m^{pre}(k)$ and a data set $C_m^{pre}(k)$, according to the equations:

$$A_m(k) = \frac{A_m^{pre}(k) - \overline{A_m^{pre}}\,\overline{C_m^{pre}}}{\overline{A_m^{pre}}}$$

and

$$C_m(k) = \frac{C_m^{pre}(k) - \overline{A_m^{pre}}\,\overline{C_m^{pre}}}{\overline{C_m^{pre}}},$$

wherein said data sets $A_m^{pre}(k)$ and $C_m^{pre}(k)$ each comprises measurements~~, error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents, where $\overline{A_m^{pre}}$ is an average of measurements~~, error-model-based transformed measurements, or logarithm-based-transformed measurements~~ of said plurality of different cellular constituents in said $A_m^{pre}(k)$, and $\overline{C_m^{pre}}$ is an average of measurements~~, error-model-based transformed measurements, or logarithm-based-transformed measurements~~ of said plurality of different cellular constituents in said $C_m^{pre}(k)$, wherein $A_m(k)$ is said first data set, wherein $A_m(k)$ comprises normalized measurements or normalized transformed measurements of said pre-experiment profile A_m^{pre}; and $C_m(k)$ is said second data set wherein $A_m(k)$ comprises normalized measurements or normalized transformed measurements of said reference profile C_m^{pre}; and wherein $\overline{A_m^{pre}}\,\overline{C_m^{pre}}$

is an average calculated according to the equation

$$\overline{A^{pre}_{m} C^{pre}_{m}} = \frac{1}{2M} \sum_{m=1}^{M} \overline{(A^{pre}_{m} + C^{pre}_{m})}.$$

27. (Previously Presented) The method of claim 26, further comprising normalizing errors of said data sets $\{ A^{pre}_{m}(k) \}$ and $\{ C^{pre}_{m}(k) \}$, respectively, according to the equations:

$$\sigma^{NA}_{m}(k) = \frac{\sigma^{preA}_{m}(k) \cdot \overline{A^{pre}_{m} C^{pre}_{m}}}{\overline{A^{pre}_{m}}}$$

and

$$\sigma^{NC}_{m}(k) = \frac{\sigma^{preC}_{m}(k) \cdot \overline{A^{pre}_{m} C^{pre}_{m}}}{\overline{C^{pre}_{m}}},$$

where $\sigma^{preA}_{m}(k)$ and $\sigma^{preC}_{m}(k)$ are the standard errors of $A^{pre}_{m}(k)$ and $C^{pre}_{m}(k)$, respectively, and $\sigma^{NA}_{m}(k)$ and $\sigma^{NC}_{m}(k)$ are normalized standard errors of $A_m(k)$ and $C_m(k)$, respectively.

28. (Previously Presented) The method of claim 27, further comprising normalizing background errors of said data sets $\{A^{pre}_{m}(k)\}$ and $\{C^{pre}_{m}(k)\}$, respectively, according to the equations:

$$bkgstd^{NA}_{m}(k) = \frac{bkgstd^{preA}_{m}(k) \cdot \overline{A^{pre}_{m} C^{pre}_{m}}}{\overline{A^{pre}_{m}}}$$

and

$$bkgstd_m^{NC}(k) = \frac{bkgstd_m^{preC}(k)\overline{A_m^{pre}}\,\overline{C_m^{pre}}}{\overline{C_m^{pre}}}$$

where $bkgstd_m^{preA}(k)$ and $bkgstd_m^{preC}(k)$ are the standard background errors of $A_m^{pre}(k)$ and $C_m^{pre}(k)$, respectively, and $bkgstd_m^{NA}(k)$ and $bkgstd_m^{NC}(k)$ are normalized standard background errors of $A_m(k)$ and $C_m(k)$, respectively.

29. (**Currently Amended**) The method of claim 28, further comprising calculating said averages $\overline{A_m^{pre}}$ and $\overline{C_m^{pre}}$ by excluding measurements~~, error model based transformed measurements, or logarithm based transformed measurements~~ of said plurality of different cellular constituents having a value among the highest 10% of said measurements~~, error model based transformed measurements, or logarithm based transformed measurements~~ of said plurality of different cellular constituents in said data sets $\{A_m^{pre}(k)\}$ and $\{C_m^{pre}(k)\}$, respectively.

30. (**Currently Amended**) A method for generating at least one error-corrected experiment profile of at least one experiment profile in a plurality of pairs of profiles $\{XA_m, XC_m\}$, XA_m being an experiment profile, XC_m being a reference profile, where m = 1, 2, ... , M, M is the number of pairs of profiles, said method comprising:

(a) processing, on a suitably programmed computer, said plurality of pairs of

profiles $\{XA_m, XC_m\}$ to obtain a plurality of pairs of processed profiles $\{PA_m, PC_m\}$, PA_m being a processed experiment profile, PC_m being a processed reference profile, wherein said processing comprises normalizing at least one said experiment profile XA_m and reference profile XC_m;

(b) calculating, on a suitably programmed computer, an average processed reference profile $\overline{PC}$ of processed reference profiles $\{PC_m\}$, where m = 1,2, ..., M;

(c) determining, on a suitably programmed computer, for at least one processed profile pair $\{PA_m, PC_m\}$ where $m \in \{1, 2, ..., M\}$ of said plurality of pairs of processed profiles $\{PA_m, PC_m\}$, where m = 1, 2, ..., M, a differential reference profile, **$PC_{diff}(m,k)$,** computed between PC_m and $\overline{PC}$ **wherein said average processed reference profile $\overline{PC}$ comprises data set $\{\overline{PC}(k)\}$;**

(d) via said differential reference profile determined for said at least one processed profile pair, removing, on a suitably programmed computer, systematic cross-experiment error from a processed experiment profile PA_m of said at least one processed profile pair $\{PA_m, PC_m\}$ where $m \in \{1, 2, ..., M\}$ to generate a first error-corrected processed experiment profile PA'_m ; wherein for each $m \in \{1, 2, ..., M\}$, said processed experiment profile PA_m comprises a first processed data set, **$\{PA_m(k)\}$,** said processed reference profile PC_m comprises a second processed data set, ~~**said average processed reference profile $\overline{PC}$ comprises data set $\{\overline{PC}(k)\}$,**~~ said first error-corrected processed experiment profile PA'_m comprises dataset $\{PA'_m(k)\}$, said experiment profile XA_m comprises data set $\{XA_m(k)\}$, said reference profile

XC_m comprises data set $\{XC_m(k)\}$, wherein said data set $\{XA_m(k)\}$ comprises measurements of a plurality of different cellular constituents measured in a sample having been subject to a first condition, said data set $\{XC_m(k)\}$ comprises measurements of said plurality of different cellular constituents measured in a sample having been subject to a second condition, and where k = 1, 2, ..., N; k is an index of measurements of cellular constituents, N being the total number of measurements, **wherein generating respective $PA'_m(k)$ of said first error-corrected processed experiment profile PA'_m comprises subtracting $PC_{gm}(m,k)$ from $PA_m(k)$**; and

~~(e) obtaining a data set $\{PA''_m(k)\}$, wherein obtaining said data set $\{PA''_m(k)\}$ comprises combining said first error-corrected processed experiment profile PA'_m with said processed experiment profile PA_m using a weighing factor $\{w(k)\}$, k = 1, 2, ..., N, wherein w(k) is a weighing factor for the k'th measurement; and~~

~~(f)~~ (e) outputting to a user, a user interface device, a computer readable storage medium, or a local or remote computer system; or displaying; said first error-corrected processed experiment profile PA'_m [[,]] or said data set $\{PA'_m(k)\}$, ~~a second error-corrected processed experiment profile PA''_m or said data set $\{PA''_m(k)\}$, wherein said second error-corrected processed experiment profile PA''_m comprises said data set $\{PA''_m(k)\}$~~.

31. (Canceled)

32. **(Currently Amended)** The method of claim 30, wherein said normalizing is carried out according to the equations:

$$NA_m(k) = \frac{XA_m(k)\cdot\overline{XAC}}{\overline{XA_m}}$$

and

$$NC_m(k) = \frac{XC_m(k)\cdot\overline{XAC}}{\overline{XC_m}}$$

where $\{NA_m(k)\}$ is said first data set of said processed experiment profile PA_m, and $\{NC_m(k)\}$ is said second data set of said processed reference profile PC_m; where $\overline{XA_m}$ is an average of measurements, ~~error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents of said data set $\{XA_m(k)\}$, and $\overline{XC_m}$ is an average of measurements, ~~error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents of data set $\{XC_m(k)\}$; and wherein $\overline{XAC}$ is an average calculated according to the equation

$$\overline{XAC} = \frac{1}{2M}\sum_{m=1}^{M}(\overline{XA_m} + \overline{XC_m}).$$

33. (Previously Presented) The method of claim 32, further comprising normalizing errors of said experiment profile XA_m and reference profile XC_m

according to the equations:

$$\sigma_m^A(k) = \frac{\sigma_m^{XA}(k)\cdot\overline{XAC}}{\overline{XA_m}}$$

and

$$\sigma_m^C(k) = \frac{\sigma_m^{XC}(k)\cdot\overline{XAC}}{\overline{XC_m}}$$

where $\sigma_m^{XA}(k)$ and $\sigma_m^{XC}(k)$ are the standard errors of $XA_m(k)$ and $XC_m(k)$, respectively, and $\sigma_m^A(k)$and $\sigma_m^C(k)$ are normalized standard errors of $NA_m(k)$ and $NC_m(k)$, respectively.

34. (Previously Presented) The method of claim 33, further comprising normalizing background errors of said experiment profile XA_m and reference profile XC_m according to the equations:

$$bkgstd_m^A(k) = \frac{bkgstd_m^{XA}(k)\cdot\overline{XAC}}{\overline{XA_m}}$$

and

$$bkgstd_m^C(k) = \frac{bkgstd_m^{XC}(k)\cdot\overline{XAC}}{\overline{XC_m}}$$

where $bkgstd_m^{XA}(k)$ and $bkgstd_m^{XC}(k)$ are the standard background errors of $XA_m(k)$ and $XC_m(k)$, respectively, and $bkgstd_m^A(k)$ and $bkgstd_m^C(k)$ are normalized standard

background errors of said $NA_m(k)$ and said $NC_m(k)$, respectively.

35. **(Currently Amended)** The method of claim 33, further comprising determining said averages $\overline{XA_m}$ and $\overline{XC_m}$ excluding measurements of said plurality of different cellular constituents having a value among the highest 10% of said measurements~~, error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents in said data sets $\{XA_m(k)\}$ and $\{XC_m(k)\}$, respectively.

36. (Previously Presented) The method of claim 30, wherein said processing step (a) comprises:

normalizing each said experiment profile XA_m and reference profile XC_m to generate normalized data set $\{NA_m(k)\}$ and normalized data set $\{NC_m(k)\}$, respectively;

transforming said normalized data set $\{NA_m(k)\}$ to obtain a transformed data set $\{TA_m(k)\}$, where said transformed data set $\{TA_m(k)\}$ is said first data set of said processed experiment profile PA_m; and

transforming said normalized data set $\{NC_m(k)\}$ to obtain a transformed data set $\{TC_m(k)\}$, where said transformed data set $\{TC_m(k)\}$ is said second data set of said processed reference profile PC_m;

wherein said transforming is carried out for an experiment according to equations

$$\overline{TA}_m(k) = f(x) = \frac{\ln\left[\frac{b^2+2\cdot a^2\cdot NA_m(k)}{a} + 2\cdot\sqrt{a^2\cdot b^2\cdot NA_m(k)+a^4\cdot[NA_m(k)]^2}\right]}{a} + d,$$

for $NA_m(k)>0$

and

$$TC_m(k) = f(x) = \frac{1}{a}\left[\frac{b^2}{2a} + 2\sqrt{c^2 + b^2 NC_m(k) + a^2 [NC_m(k)]^2}\right] + d,$$

for $NC_m(k)>0$

where d is described by equation

$$d = \frac{-1}{a}\left[\frac{b^2}{2a} + 2c\right]$$

and where a is the fractional error coefficient of said experiment, b is the Poisson error coefficient of said experiment, and c is the standard deviation of background noise of said experiment.

37. (Canceled)

38. (Previously Presented) The method of claim 30, wherein said processing step (a) comprises:

normalizing each said experiment profile XA_m and reference profile XC_m to generate normalized data set $\{NA_m(k)\}$ and normalized data set $\{NC_m(k)\}$, respectively;

transforming said normalized data set $\{NA_m(k)\}$ to a new domain in which variance becomes a constant to obtain a transformed data set $\{TA_m(k)\}$;

transforming said normalized data set $\{NC_m(k)\}$ to the new domain in which variance becomes a constant to obtain a transformed data set $\{TC_m(k)\}$; and

removing nonlinearity from each said transformed data sets $\{TA_m(k)\}$ and $\{TC_m(k)\}$, respectively.

39. (Previously Presented) The method of claim 38, wherein said removing nonlinearity is carried out by a method comprising

(a1) calculating an average transformed profile of transformed experiment profiles and transformed reference profiles, wherein each of said transformed experiment profiles contains a corresponding transformed data set $\{TA_m(k)\}$, and each of said transformed reference profiles contains a corresponding transformed data set $\{TC_m(k)\}$; and

(a2) calculating first differences between each of said transformed experiment profiles and said average transformed profile; calculating second differences between each of said transformed reference profiles and said average transformed profile; adjusting, wherein the adjusting corrects nonlinearity, each of said transformed experiment profiles based on said first differences between each of said transformed experiment profiles and said average transformed profile, and adjusting, wherein the adjusting corrects nonlinearity, each of said transformed reference profiles based on said second differences between each of said transformed reference profiles and said average transformed profile.

40. (**Currently Amended**) The method of claim 39, further comprising calculating said first differences based on the differences in a first subset of ~~error-~~

~~model-based-transformed-measurements-or-logarithm-based~~ transformed measurements of said plurality of different cellular constituents between each of said transformed experiment profiles and said average transformed profile, and calculating said second differences based on the differences in a second subset of transformed measurements of said plurality of different cellular constituents between each of said transformed reference profiles and said average transformed profile.

41. (**Currently Amended**) The method of claim 40, wherein each said first subset consists of ~~error-model-based-transformed-measurements-or-logarithm-based~~ transformed measurements that are ranked similarly between each of said transformed experiment profiles and said average transformed profile, and each said second subset consists of ~~error-model-based-transformed-measurements-or-logarithm-based~~ transformed measurements that are ranked similarly between each of said transformed reference profiles and said average transformed profile.

42. (**Currently Amended**) The method of claim 41, wherein said adjusting step (a2) is carried out by a method comprising:

(a2i) binning said first subset into a plurality of bins, each said bin consisting of ~~error-model-based-transformed-measurements-or-logarithm-based~~ transformed measurements of said plurality of different cellular constituents in one of said transformed experiment profiles and said average transformed profile having a value in a given range; and binning said second subset into a plurality of bins, each said bin

consisting of ~~error-model-based transformed measurements, or logarithm based~~ transformed measurements of said plurality of different cellular constituents in one of said transformed reference profiles and said average transformed profile having a value in a given range;

(a2ii) calculating, in each bin of said plurality of bins, a first mean difference between a feature value of ~~error-model-based transformed measurements or logarithm based~~ transformed measurements of said plurality of different cellular constituents in said one of said transformed experiment profiles and a feature value of said average transformed profile, and calculating a second mean difference between a feature value of transformed measurements of said plurality of different cellular constituents in said one of said reference profiles and a feature value of the average profile;

(a2iii) determining a first curve of said first mean difference as a first function of values of ~~error-model-based transformed measurements or logarithm based~~ transformed measurements of said plurality of different cellular constituents for said one of said transformed experiment profiles, wherein said first function is represented by, $nonlinear\_TA_m$, and determining a second curve of said second mean difference as a second function of values of transformed measurements of said plurality of different cellular constituents for said one of said transformed reference profiles, wherein said second function is represented by $nonlinear\_TC_m$; and

(a2iv) computing corrected transformed measurements of said plurality of different cellular constituents in each said transformed data set $\{TA_m(k)\}$, according to

the equation:

$$TA_m^{corr}(k) = TA_m(k) - nonlinear\_TA_m(k),$$

and computing corrected transformed measurements of said plurality of different cellular constituents in each said transformed data set $\{TC_m(k)\}$, according to the equation:

$$TC_m^{corr}(k) = TC_m(k) - nonlinear\_TC_m(k),$$

where k = 1, ..., N; and where $\{TA_m^{corr}(k)\}$ is said first processed data set of said processed experiment profile PA_m, and $\{TC_m^{corr}(k)\}$ is said second processed data set of said processed reference profile PC_m.

43. (**Currently Amended**) The method of claim 42, wherein said processed experiment profile PA_m and said processed reference profile PC_m comprise ~~error-model-based transformed measurements or logarithm based~~ transformed measurements of said plurality of different cellular constituents from the same experimental reaction.

44. (**Currently Amended**) The method of claim 43, further comprising calculating $\overline{PC}(k)$ according to the equation

$$\overline{PC}(k) = \frac{1}{M}\sum_{m=1}^{M} PC_m(k),$$

wherein $\{PC_m(k)\}$ comprises ~~error-model-based transformed measurements or logarithm based~~ transformed measurements from said second processed data

set $\{TC_m^{corr}(k)\}$ and calculating said differential reference profile according to the equation

$$PC_{diff}(m,k) = PC_m(k) - \overline{PC}(k)$$

and wherein said first error-corrected profile is calculated according to the equation

$$PA'_m(k) = PA_m(k) - PC_{diff}(m,k),$$

wherein $\{PA_m(k)\}$ comprises ~~error-model-based-transformed-measurements or logarithm-based~~ transformed measurements from said first data set $\{TA_m^{corr}(k)\}$.

45. (Previously Presented) The method of claim 44, further comprising

(d) calculating for each processed profile pair $\{PA_m, PC_m\}$, where m $\in \{1, 2, ..., M\}$, a second error-corrected experiment profile PA''_m comprising data set $\{PA''_m(k)\}$ by combining said first error-corrected experiment profile PA'_m with said processed experiment profile PA_m using a weighing factor $\{w(k)\}$, k = 1,2, ..., N, wherein $w(k)$ is a weighing factor for the kth measurement.

46. (Previously Presented) The method of claim 45, wherein said second error-corrected experiment profile PA''_m is calculated according to the equation

$$PA''_m(k) = (1-w(k)) \cdot PA_m(k) + w(k)PA'_m(k).$$

47. (Previously Presented) The method of claim 46, further comprising determining said weighing factor according to the equation

$$w(k) = 1 - e^{-a.s\left[\frac{\overline{PA}(k)}{avg\_bkgstd}\right]^2}$$

where *avg_bkgstd* is an average background standard error.

48. (Previously Presented) The method of claim 47, further comprising determining said *avg_ bkgstd* according to the equation

$$avg\_bkgstd = \frac{1}{N}\sum_{k=1}^{N}\left[\frac{1}{M}\sum_{m=1}^{M} bkgstd(m,k)\right]$$

where *bkgstd (m, k)* is background standard error of $PC_m(k)$.

49. (Previously Presented) The method of claim 44, further comprising determining errors $\{P\sigma'_m\}$ of said first error-corrected experiment profile $\{PA'_m\}$, wherein said $\{P\sigma'_m\}$ comprises error data set $\{P\sigma'_m(k)\}$.

50. (Previously Presented) The method of claim 49, further comprising determining said error data set $\{P\sigma'_m(k)\}$ according to the equation

$$\sigma'_m(k) = \sqrt{P\sigma_m^2(k) + mixed\_P\sigma_m^2(k) - 2Cor(k)\cdot P\sigma_m(k)\cdot mixed\_P\sigma_m(k)}$$

where $P\sigma_m(k)$ is the standard error of $A_m(k)$, and determining $mixed\_P\sigma_m(k)$ according to the equation

$$mixed\_P\sigma_m(k) = \frac{P\sigma_m(k)*(M-1)P\sigma_{ref}(k)}{M}$$

where

$$P\sigma_{ref}(k) = \sqrt{\frac{1}{M-1}\sum_{m}^{M}(PC_m(k) - \overline{PC}(k))^2}$$

and where Cor(k) is a correlation coefficient between said processed experiment profile PA_m and said processed reference profile PC_m.

51. (Previously Presented) The method of claim 50, wherein said Cor(k) is determined according to the equation

$$Cor(k) = CorMax \cdot \left[1 - e^{-0.5\left[\frac{PC(k)}{\sigma_{PC}(k)\,Sigma}\right]^2}\right]$$

where CorMax is a number between 0 and 1.

52. (Previously Presented) The method of claim 51, further comprising determining errors $\{P\sigma''_m\}$ of said second error-corrected experiment profile $\{PA''_m\}$ wherein said $\{P\sigma''_m\}$ comprises error data set $\{P\sigma''_m(k)\}$.

53. (Previously Presented) The method of claim 52, further comprising determining said error data set $\{P\sigma''_m(k)\}$ according to the equation

$$P\sigma''_m(k) = \sqrt{[1 - w(k)] \cdot P\sigma^2_m(k) + w(k)P\sigma'^2_m(k)}$$

where $P\sigma_m(k)$ is the standard error of $PA_m(k)$, and further comprising determining $P\sigma'_m(k)$ according to the equation

$$Pa'_m(k) = \sqrt{Pa_m^2(k) + mixed\_Pa_m^2(k) - 2 \cdot Cor(k) \cdot Pa_m(k) \cdot mixed\_Pa_m(k)},$$

and

further comprising determining $mixed\_Pa_m(k)$ according to the equation

$$mixed\_Pa_m(k) = \frac{Pa_m(k) + (M-1) \cdot Pa_{ref}(k)}{M}$$

where

$$Pa_{ref}(k) = \sqrt{\frac{1}{M-1} \sum_{m}^{M} (PC_m(k) - \overline{PC}(k))^2}$$

and where Cor(k) is a correlation coefficient between said processed experiment profile PA_m and said processed reference profile PC_m.

54. (Previously Presented) The method of claim 53, further comprising determining said Cor(k) according to the equation

$$Cor(k) = CorMax \cdot \left[1 - e^{-0.5\left[\frac{PC(k)}{corg\_Diagonal}\right]^2}\right]$$

where CorMax is a number between 0 and 1.

55. (Previously Presented) The method of claim 54, wherein each said pair of profiles XA_m and XC_m comprise measurements of said plurality of different cellular constituents from a two-channel microarray experiment.

56. (Previously Presented) The method of claim 55, wherein said reference

profiles $\{XC_m\}$, m = 1, 2, ... , M, are measured with samples labeled with a same label.

57. (Previously Presented) The method of claim 56, wherein at least one of said pairs of profiles $\{XA_m, XC_m\}$ is a virtual profile.

58. (Canceled)

59. (Canceled)

60. (Canceled)

61. (Canceled)

62. (Canceled)

63. (Canceled)

64. (Canceled)

65. (Canceled)

66. (**Currently Amended**) A method for generating at least one error-corrected experiment profile of at least one experiment profile A_m, where $m \in \{1, 2, ..., M\}$ in at least one of a plurality of pairs of profiles $\{A_m, C_m\}$, A_m being an experiment profile, C_m being a reference profile, where m = 1, 2, ... , M, M is the number of pairs of profiles, said method comprising:

via a differential reference profile **$C_{dif}(m,k)$** calculated between C_m and an average reference profile **$\bar{C}$**, **wherein said average reference profile $\bar{C}$ comprises data set $\{\bar{C}(k)\}$,** removing, on a suitably programmed computer, systematic cross-

experiment error from said experiment profile A_m for profile pair $\{A_m, C_m\}$ where m $\in$ {1, 2, ... , M} to generate a first error-corrected experiment profile A'_m; wherein said average reference profile $\bar{C}$ is an average of reference profiles $\{C_m\}$, m = 1, 2, ... , M; wherein for each m $\in$ {1, 2, ..., M}, said first error-corrected experiment profile A'_m comprises data set $\{A'_m(k)\}$, said experiment profile A_m comprises data set $\{A_m(k)\}$, **and** said reference profile C_m comprises data set $\{C_m(k)\}$, ~~**and said average reference profile $\bar{C}$ comprises data set $\{\bar{C}(k)\}$,**~~ wherein said data set $\{A_m(k)\}$ comprises measurements~~**, error-model-based-transformed measurements, or logarithm-based transformed measurements**~~ of a plurality of different cellular constituents measured in a sample having been subject to a first condition, said data set $\{C_m(k)\}$ comprises measurements~~**, error-model-based transformed measurements, or logarithm-based transformed measurements**~~ of said plurality of different cellular constituents measured in a sample having been subject to a second condition, wherein k = 1, 2, ... , N; k is an index of measurements~~**, error-model-based transformed measurements, or logarithm-based transformed measurements**~~ of cellular constituents, N being the total number of measurements**, wherein generating respective $A'_m(k)$ of said first error-corrected experiment profile A'_m comprises subtracting $C_{error}(m,k)$ from $A_m(k)$:**

~~**obtaining a data set $\{A''_m(k)\}$, wherein obtaining said data set $\{A''_m(k)\}$ comprises combining said first error-corrected experiment profile A'_m with said experiment profile A_m using a weighing factor $\{w(k)\}$, k = 1, 2, ... , N, wherein $w(k)$ is a weighing factor for the k^{th} measurement;**~~ and

outputting to a user, a user interface device, a computer readable storage medium, or a local or remote computer system; or displaying: said first error-corrected experiment profile $A'_m[[,]]$ or said data set $\{A'_m(k)\}$, ~~a second error-corrected experiment profile A''_m, or said data set $\{A''_m(k)\}$, wherein said second error-corrected experiment profile A''_m comprises said data set $\{A''_m(k)\}$~~.

67. (Previously Presented) The method of claim 18, further comprising obtaining said transformed measurements of said data set $\{A_m(k)\}$ and said data set $\{C_m(k)\}$ for an experiment according to the equations:

$$A_m(k) = f(x) = \frac{\ln\left[\frac{a^2+2\cdot a^2\cdot XA_m(k)}{a} + 2\sqrt{a^2+b^2\cdot XA_m(k)+a^2\cdot[XA_m(k)]^2}\right]}{a} + d,$$

for $XA_m(k)>0$

and

$$C_m(k) = f(x) = \frac{\ln\left[\frac{a^2+2\cdot a^2\cdot XC_m(k)}{a} + 2\sqrt{a^2+b^2\cdot XC_m(k)+a^2\cdot[XC_m(k)]^2}\right]}{a} + d,$$

for $XC_m(k)>0$

where $\{XA_m(k)\}$ and $\{XC_m(k)\}$ are data sets comprising measurements of said plurality of different cellular constituents that when transformed produce said transformed measurements of said plurality of different cellular constituents of said data set $A_m(k)$ and said data set $C_m(k)$, respectively, where d is described by the equation:

$$d = \frac{-3n\left[\frac{A^2}{B}+3-c\right]}{a}$$

and where a is the fractional error coefficient of said experiment, b is the Poisson error coefficient of said experiment, and c is the standard deviation of background noise of said experiment.

68. (Canceled)

69. (Canceled)

70. (Previously Presented) The method of claim 30, wherein said processing comprises:

normalizing, transforming, and/or removing nonlinearity from measurements of said plurality of cellular constituents of said data set $\{XA_m(k)\}$ of said experiment profile XA_m, and from measurements of said plurality of cellular constituents of said data set $\{XC_m(k)\}$ of said reference profile XC_m.

71. **(Currently Amended)** A computer program product for use in conjunction with a computer having a processor and a memory connected to the processor, said computer program product comprising a computer readable storage medium having a computer program mechanism encoded thereon, wherein said computer program mechanism may be loaded into the memory of said computer and

cause said computer to carry out a method for generating at least one error-corrected experiment profile of at least one experiment profile in a plurality of pairs of profiles $\{A_m,C_m\}$, where m = 1,2, …, M, and M is the number of the pairs of profiles; and wherein, for each m ∈ {1, 2, …, M}, A_m is an experiment profile, and C_m is a reference profile; and wherein $\{A_m\}$ represents experiment profiles in said plurality of pairs of profiles $\{A_m,C_m\}$ and $\{C_m\}$ represents reference profiles in said plurality of pairs of profiles $\{A_m, C_m\}$, said method comprising:

(a) calculating, on a computer, an average reference profile $\bar{C}$ of said plurality of reference profiles $\{C_m\}$ where m = 1, 2, …, M;

(b) determining, on a computer, for at least one profile pair $\{A_m,C_m\}$ where m ∈ {1, 2, …, M} of said plurality of pairs of profiles $\{A_m, C_m\}$ a differential reference profile $C_{diff}(m,k)$ computed between C_m and $\bar{C}$, **wherein said average reference profile $\bar{C}$ comprises data set $\{\bar{C}(k)\}$**;

(c) via said differential reference profile determined for said profile pair, removing, on a computer, systematic cross-experiment error from an experiment profile A_m of said at least one profile pair $\{A_m, C_m\}$ where m ∈ {1, 2, …, M} to generate a first error-corrected experiment profile A'_m for each m ∈ {1, 2, …, M}, wherein said experiment profile A_m comprises a first data set $\{A_m(k)\}$, said reference profile C_m comprises a second data set, ~~said average reference profile $\bar{C}$ comprises data set $\{\bar{C}(k)\}$~~, and said first error-corrected experiment profile A'_m comprises data set $\{A'_m(k)\}$; wherein said first data set comprises measurements, ~~error-model-based transformed~~

~~measurements, or logarithm-based transformed measurements~~ of a plurality of different cellular constituents measured in a sample having been subject to a first condition, said second data set comprises measurements~~, error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents measured in a sample having been subject to a second condition; and wherein k = 1, 2, ..., N; k is an index of measurements, ~~error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents, N being the total number of measurements, ~~error-model-based transformed measurements, or logarithm-based transformed measurements~~, wherein generating respective $A'_m(k)$ of said first error-corrected experiment profile A'_m comprises subtracting $\mathcal{E}_{e(s)}(m,k)$ from $A_m(k)$:

~~(d) obtaining a data set $\{A''_m(k)\}$ by combining said first error-corrected experiment profile A'_m with said experiment profile A_m using a weighing factor $\{w(k)\}$, k = 1, 2, ... , N, wherein $w(k)$ is a weighing factor for the k-th measurement;~~ and

~~(e)~~ (d) outputting to a user, a user interface device, a computer readable storage medium, or a local or remote computer system; or displaying: said first error-corrected experiment profile $A'_m[[,]]$ or said data set $\{A'_m(k)\}$, ~~a second error-corrected experiment profile A''_m, or said data set $\{A''_m(k)\}$, wherein said second error-corrected experiment profile A''_m comprises said data set $\{A''_m(k)\}$~~.

72. (Previously Presented) The computer program product of claim 71, wherein said steps (b) and (c) are performed for each profile pair $\{A_m, C_m\}$ where $m \in \{1, 2, \ldots, M\}$.

73. **(Currently Amended)** The computer program product of claim 72, wherein each of said experiment profile A_m and said reference profile C_m comprises measurements~~, error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents from the same experimental reaction.

74. (Previously Presented) The computer program product of claim 73, wherein said $\bar{C}(k)$ is calculated according to the equation

$$\bar{C}(k) = \frac{1}{M} \sum_{m=1}^{M} C_m(k)$$

wherein said differential reference profile is determined according to the equation

$$C_{diff}(m,k) = C_m(k) - \bar{C}(k)$$

and wherein said first error-corrected experiment profile A'_m is generated according to the equation

$$A'_m(k) = A_m(k) - C_{diff}(m,k)$$

wherein $\{A_m(k)\}$ is said first data set of experiment profile A_m.

75. (**Currently Amended**) The computer program product of claim 74, wherein the method further comprises:

~~(d)~~ (e) calculating, for one or more remaining profile pairs out of said profile pairs $\{A_m, C_m\}$, a respective second error-corrected experiment profile A''_m; and

~~(e)~~ (f) outputting to, a user interface device, a computer readable storage medium, or a local or remote computer system; or displaying; said respective second error-corrected experiment profile A''_m or ~~said~~ a data set $\{A''_m(k)\}$.

76. (Previously Presented) The computer program product of claim 75, wherein said second error-corrected experiment profile A''_m is calculated according to the equation

$$A''_m(k) = (1-w(k)) \cdot A_m(k) + w(k) \cdot A'_m(k).$$

77. (**Currently Amended**) The computer program product of claim 76, wherein the method further comprises determining **said** a weighing factor $w(k)$ according to the equation

$$w(k) = 1 - e^{-0.5\left[\frac{2\,avg\_bkgstd}{low\_sig(k)}\right]^2}$$

where *avg_bkgstd* is an average background standard error.

78. (Previously Presented) The computer program product of claim 77,

wherein the method further comprises determining said *avg_bkgstd* according to the equation

$$avg\_bkgstd = \frac{1}{N}\sum_{k=1}^{N}\left[\frac{1}{M}\sum_{m=1}^{M} bkgstd(m,k)\right]$$

where *bkgstd (m, k)* is background standard error of $C_m(k)$.

79. (Previously Presented) The computer program product of claim 74, wherein the method further comprises determining errors $\{\sigma'_m(k)\}$ of said data set $\{A'_m(k)\}$ in said first error-corrected experiment profile A'_m.

80. (Previously Presented) The computer program product of claim 79, wherein the method further comprises determining said errors $\{\sigma'_m(k)\}$ according to the equation

$$\sigma'_m(k) = \sqrt{\sigma_m^2(k) + mixed\_\sigma_m^2(k) - 2\cdot Cor(k)\cdot\sigma_m(k)\cdot mixed\_\sigma_m(k)}$$

where $\sigma_m(k)$ is the standard error of $A_m(k)$, the method further comprising determining $mixed\_\sigma_m(k)$ according to the equation

$$mixed\_\sigma_m(k) = \frac{\sigma_m(k)+(M-1)\sigma_{ref}(k)}{M}$$

where $\sigma_{ref}(k) = \sqrt{\frac{1}{M-1}\sum_{m}^{M}(C_m(k)-\bar{C}(k))^2}$

and where Cor(k) is a correlation coefficient between said experiment profile A_m and said reference profile C_m.

81. (Previously Presented) The computer program product of claim 80, wherein the method further comprises determining said Cor(k) according to the equation

$$Cor(k) = CorMax \cdot \left[1 - e^{-0.5 \cdot \left[\frac{\tau(k)}{mag\_Rkgated}\right]^2}\right]$$

where CorMax is a number between 0 and 1.

82. (Previously Presented) The computer program product of claim 77, wherein the method further comprises determining errors $\{\sigma''_m(k)\}$ of said data set $\{A''_m(k)\}$ in said second error-corrected experiment profile A''_m.

83. (Previously Presented) The computer program product of claim 82, wherein said errors $\{\sigma''_m(k)\}$ are determined according to the equation

$$\sigma''_m(k) = \sqrt{[1 - w(k)] \cdot \sigma_m^2(k) + w(k)\sigma'^2_m(k)}$$

where $\sigma_m(k)$ is the standard error of $A_m(k)$, the method further comprising (i) determining $\sigma'_m(k)$ according to the equation

$$\sigma'_m(k) = \sqrt{\sigma_m^2(k) + mixed\_\sigma_m^2(k) - 2 \cdot Cor(k) \cdot \sigma_m(k) \cdot mixed\_\sigma_m(k)}, \text{ and}$$

(ii) determining $mixed\_\sigma_m(k)$ according to the equation

$$mixed\_\sigma_m(k) = \frac{\sigma_m(k) + (M-1)\cdot\sigma_{ref}(k)}{M}$$

where $\sigma_{ref}(k) = \sqrt{\frac{1}{M-1}\sum_{m}^{M}(c_m(k) - \bar{C}(k))^2}$

and where Cor(k) is a correlation coefficient between said experiment profile A_m and said reference profile C_m.

84. (Previously Presented) The computer program product of claim 83, wherein the method further comprises determining said Cor(k) according to the equation

$$Cor(k) = CorMax \cdot \left[1 - e^{-0.5\left[\frac{\bar{C}(k)}{\sigma_{ref}(k)}\right]^2}\right]$$

where CorMax is a number between 0 and 1.

85. (Previously Presented) The computer program product of claim 72, wherein said experiment profile A_m and said reference profile C_m of each said profile pair $\{A_m, C_m\}$ are measured in a two-channel microarray experiment.

86. (Previously Presented) The computer program product of claim 85, wherein said reference profiles $\{C_m\}$, where m = 1, 2, ... , M_c are measured with samples labeled with a same label.

87. (Previously Presented) The computer program product of claim 72, wherein at least one of said plurality of pairs of profiles $\{A_m, C_m\}$ is a virtual profile.

88. (**Currently Amended**) The computer program product of claim 71, wherein said plurality of pairs of profiles $\{A_m, C_m\}$ are transformed profiles each comprising ~~error-model-based transformed measurements or logarithm-based~~ transformed measurements of said plurality of different cellular constituents in data set $\{A_m(k)\}$ and data set $\{C_m(k)\}$, respectively; and wherein said data set $\{A_m(k)\}$ is said first data set, and said data set $\{C_m(k)\}$ is said second data set.

89. (**Currently Amended**) The computer program product of claim 71, wherein the method further comprises:

(a0) removing nonlinearity, prior to said calculating step (a), from measurements, ~~error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents to generate said plurality of pairs of profiles $\{A_m, C_m\}$ comprising said experiment profile A_m and reference profile C_m.

90. (**Currently Amended**) The computer program product of claim 89, wherein said removing step (a0) comprises:

(a0i) calculating an average profile of pre-experiment profiles $\{A_m^{pre}\}$ and pre- reference profiles $\{C_m^{pre}\}$; wherein each of said pre-experiment profiles

comprises measurements, ~~error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents measured in said sample having been subject to said first condition, which when nonlinearity is removed therefrom, produces each said experiment profile A_m; and wherein each of said pre-reference profiles comprises measurements, ~~error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents measured in said sample having been subject to said second condition, which when nonlinearity is removed therefrom, produces each said reference profile C_m; and

(a0ii) calculating first differences between each of said pre-experiment profiles $\{A_m^{pre}\}$ and said average profile; calculating second differences between each of said pre-reference profiles $\{C_m^{pre}\}$ and said average profile; adjusting, wherein the adjusting comprises correcting nonlinearity, each of said pre-experiment profiles $\{A_m^{pre}\}$ based on said first differences between each of said pre-experiment profiles $\{A_m^{pre}\}$ and said average profile, thereby generating each said experiment profile A_m; and adjusting, wherein the adjusting comprises correcting nonlinearity, each of pre-reference profiles $\{C_m^{pre}\}$ based on said second differences between each of said pre-reference profiles $\{C_m^{pre}\}$ and said average profile, thereby generating each said reference profile C_m.

91. **(Currently Amended)** The computer program product of claim 90, wherein the method further comprises calculating said first differences based on a first subset of said measurements~~, error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents in said pre-experiment profiles $\{A_m^{pre}\}$ and said average profile; and calculating said second differences based on a second subset of said measurements~~, error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents in said pre-reference profiles $\{C_m^{pre}\}$ and said average profile.

92. **(Currently Amended)** The computer program product of claim 91, wherein said first subset consists of measurements~~, error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents that are ranked similarly between each of said pre-experiment profiles $\{A_m^{pre}\}$ and said average profile, and said second subset consists of measurements~~, error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents that are ranked similarly between each of said pre-reference profiles $\{C_m^{pre}\}$ and said average profile.

93. **(Currently Amended)** The computer program product of claim 92,

wherein said adjusting step (a0ii) is carried out by a method comprising:

(ii1) binning said first subset into a first plurality of bins, wherein each of said first plurality of bins consists of measurements, ~~error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents in one of said pre-experiment profiles $\{A_m^{pre}\}$ and said average profile having a value in a given range; and binning said second subset into a second plurality of bins, wherein each of said second plurality of bins consists of measurements, ~~error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents in one of said pre-reference profiles $\{C_m^{pre}\}$ and said average profile having a value in a given range;

(ii2) calculating, in each bin of said first plurality of bins, a first mean difference between a feature value of measurements, ~~error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said one of said pre-experiment profiles $\{A_m^{pre}\}$ and a feature value of said average profile, and calculating a second mean difference between a feature value of measurements, ~~error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said one of said pre-reference profiles $\{C_m^{pre}\}$ and a feature value of said average profile;

(ii3) determining a first curve of said first mean difference as a first function of values of measurements, ~~error-model-based transformed measurements, or~~

~~logarithm-based transformed measurements~~ of said plurality of different cellular constituents for said one of said pre-experiment profiles $\{A_m^{pre}\}$, wherein said first function is represented by, *nonlinear* $\_A_m^{pre}$; and determining a second curve of said second mean difference as a second function of values of measurements, ~~error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents for said one of said pre-reference profiles $\{C_m^{pre}\}$, wherein said second function is represented by *nonlinear* $\_C_m^{pre}$; and

(ii4) adjusting each of said pre-experiment profiles $\{A_m^{pre}\}$ according to the equation:

$$A_m(k) = A_m^{pre}(k) - nonlinear\_A_m^{pre}(k),$$

and adjusting each of said pre-reference profiles $\{C_m^{pre}\}$ according to the equation:

$$C_m(k) = C_m^{pre}(k) - nonlinear\_C_m^{pre}(k),$$

where k = 1, ... , N; and where $A_m^{pre}(k)$ and $C_m^{pre}(k)$ are data sets of each of said pre-experiment profiles $\{A_m^{pre}\}$ and each of said pre-reference profiles $\{C_m^{pre}\}$, respectively; and where $A_m(k)$ and $C_m(k)$ are said first data set and said second data set, respectively.

94. **(Currently Amended)** The computer program product of claim 71,

wherein the method further comprises:

(a0) normalizing, prior to said calculating step (a), measurements~~, error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents in a pre-experiment profile A_m^{pre} and a pre-reference profile C_m^{pre} to generate said experiment profile A_m and said reference profile C_m, respectively.

95. **(Currently Amended)** The computer program product of claim 94, wherein said normalizing step (a0) comprises normalizing a data set $A_m^{pre}(k)$ and a data set $C_m^{pre}(k)$, according to the equations:

$$A_m(k) = \frac{A_m^{pre}(k) - \overline{A_m^{pre}}}{\overline{A_m^{pre}}}$$

and

$$C_m(k) = \frac{C_m^{pre}(k) - \overline{C_m^{pre}}}{\overline{C_m^{pre}}},$$

wherein said data sets $A_m^{pre}(k)$ and $C_m^{pre}(k)$ each comprises measurements~~, error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents, where $\overline{A_m^{pre}}$ is an average of measurements~~, error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents in said $A_m^{pre}(k)$, and $\overline{C_m^{pre}}$ is an average of measurements~~, error-model-~~

~~based-transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents in said $C_m^{pre}(k)$, wherein $A_m(k)$ is said first data set, wherein $A_m(k)$ comprises normalized measurements or normalized transformed measurements of said pre-experiment profile A_m^{pre}; and $C_m(k)$ is said second data set wherein $A_m(k)$ comprises normalized measurements or normalized transformed measurements of said reference profile C_m^{pre}; and wherein $\overline{A_m^{pre} C_m^{pre}}$ is an average calculated according to the equation

$$\overline{A_m^{pre} C_m^{pre}} = \frac{1}{2M} \sum_{m=1}^{M} (\overline{A_m^{pre}} + \overline{C_m^{pre}}).$$

96. (Previously Presented) The computer program product of claim 95, wherein the method further comprises normalizing errors of said data sets $\{ A_m^{pre}(k) \}$ and $\{ C_m^{pre}(k) \}$, respectively, according to the equations:

$$\sigma_m^{NA}(k) = \frac{\sigma_m^{preA}(k) \overline{A_m^{pre} C_m^{pre}}}{\overline{A_m^{pre}}}$$

and

$$\sigma_m^{NC}(k) = \frac{\sigma_m^{preC}(k) \overline{A_m^{pre} C_m^{pre}}}{\overline{C_m^{pre}}},$$

where $\sigma_m^{preA}(k)$ and $\sigma_m^{preC}(k)$ are the standard errors of $A_m^{pre}(k)$ and $C_m^{pre}(k)$, respectively, and $\sigma_m^{NA}(k)$ and $\sigma_m^{NC}(k)$ are normalized standard errors of $A_m(k)$ and

$C_m(k)$, respectively.

97. (Previously Presented) The computer program product of claim 96, wherein the method further comprises normalizing background errors of said data sets $\{A^{pre}_m(k)\}$ and $\{C^{pre}_m(k)\}$, respectively, according to the equations:

$$bkgstd\ ^{NA}_{m}(k) = \frac{bkgstd\ ^{preA}_{m}(k)\,\overline{A}^{pre}_{m}\,\overline{C}^{pre}_{m}}{A^{pre}_{m}}$$

and

$$bkgstd\ ^{NC}_{m}(k) = \frac{bkgstd\ ^{preC}_{m}(k)\,\overline{A}^{pre}_{m}\,\overline{C}^{pre}_{m}}{C^{pre}_{m}}$$

where $bkgstd\ ^{preA}_{m}(k)$ and $bkgstd\ ^{preC}_{m}(k)$ are the standard background errors of $A^{pre}_{m}(k)$ and $C^{pre}_{m}(k)$, respectively, and $bkgstd\ ^{NA}_{m}(k)$ and $bkgstd\ ^{NC}_{m}(k)$ are normalized standard background errors of $A_m(k)$ and $C_m(k)$, respectively.

98. (**Currently Amended**) The computer program product of claim 97, wherein the method further comprises calculating said averages $\overline{A}^{pre}_{m}$ and $\overline{C}^{pre}_{m}$ by excluding measurements~~, error-model-based-transformed-measurements, or logarithm-based-transformed-measurements~~ of said plurality of different cellular constituents having a value among the highest 10% of said measurements~~, error-model-based-transformed-measurements, or logarithm-based-transformed measurements~~ of said plurality of different cellular constituents in said data sets

$\{A_m^{pre}(k)\}$ and $\{C_m^{pre}(k)\}$, respectively.

99. **(Currently Amended)** A computer program product for use in conjunction with a computer having a processor and a memory connected to the processor, said computer program product comprising a computer readable storage medium having a computer program mechanism encoded thereon, wherein said computer program mechanism may be loaded into the memory of said computer and cause said computer to carry out a method for generating at least one error-corrected experiment profile of at least one experiment profile in a plurality of pairs of profiles $\{XA_m, XC_m\}$, XA_m being an experiment profile, XC_m being a reference profile, where m = 1, 2, ... , M, M is the number of pairs of profiles, said method comprising:

(a) processing, on a computer, said plurality of pairs of profiles $\{XA_m, XC_m\}$ to obtain a plurality of pairs of processed profiles $\{PA_m, PC_m\}$, PA_m being a processed experiment profile, PC_m being a processed reference profile, wherein said processing comprises normalizing at least one said experiment profile XA_m and reference profile XC_m;

(b) calculating, on a computer, an average processed reference profile $\overline{PC}$ of processed reference profiles $\{PC_m\}$, where m = 1,2, ..., M;

(c) determining, on a computer, for at least one processed profile pair $\{PA_m, PC_m\}$ where $m \in \{1, 2, ..., M\}$ of said plurality of pairs of processed profiles $\{PA_m,$

PC_m}, where m = 1, 2, ..., M, a differential reference profile **$PC_{diff}(m,k)$** computed between PC_m and $\overline{PC}$ **wherein said average processed reference profile $\overline{PC}$ comprises data set {$\overline{PC}$ (k)}**;

(d) via said differential reference profile determined for said at least one processed profile pair, removing, on a computer, systematic cross-experiment error from a processed experiment profile PA_m of said at least one processed profile pair {PA_m, PC_m} where m ∈ {1, 2, ..., M} to generate a first error-corrected processed experiment profile PA'_m; wherein for each m ∈ {1, 2, ..., M}, said processed experiment profile PA_m comprises a first processed data set **{$PA_m(k)$}**, said processed reference profile PC_m comprises a second processed data set, ~~**said average processed reference profile $\overline{PC}$ comprises data set {$\overline{PC}$ (k)}**~~, said first error-corrected processed experiment profile PA'_m comprises dataset {PA'_m (k)}, said experiment profile XA_m comprises data set {XA_m(k)}, said reference profile XC_m comprises data set {XC_m(k)}, wherein said data set {XA_m(k)} comprises measurements of a plurality of different cellular constituents measured in a sample having been subject to a first condition, said data set {XC_m(k)} comprises measurements of said plurality of different cellular constituents measured in a sample having been subject to a second condition, and where k = 1, 2, ..., N; k is an index of measurements of cellular constituents, N being the total number of measurements, **wherein generating respective PA'_m(k) of said first error-corrected processed experiment profile PA'_m comprises subtracting $PC_{diff}(m,k)$**

from $PA_m(k)$; and;

~~(c) obtaining data set $\{PA''_m(k)\}$, wherein obtaining said data set $\{PA''_m(k)\}$ comprises combining said first error-corrected processed experiment profile PA'_m with said processed experiment profile PA_m using a weighing factor $\{w(k)\}$, k = 1, 2, ..., N, wherein w(k) is a weighing factor for a k'th measurement; and~~

~~(d)~~ (c) outputting to a user, a user interface device, a computer readable storage medium, or a local or remote computer system; or displaying: said first error-corrected processed experiment profile PA'_m [[,]] or said data set $\{PA'_m(k)\}$, ~~a second error-corrected processed experiment profile PA''_m or said data set $\{PA''_m(k)\}$, wherein said second error-corrected processed experiment profile PA''_m comprises said data set $\{PA''_m(k)\}$~~.

100. (Previously Presented) The computer program product of claim 99, wherein said processing step (a) comprises normalizing each said experiment profile XA_m and reference profile XC_m.

101. (Currently Amended) The computer program product of claim 100, wherein said normalizing is carried out according to the equations:

$$NA_m(k) = \frac{xA_m(k) \cdot xAc}{xA_m}$$

and

$$NC_m(k) = \frac{XC_m(k) - \overline{XAC}}{\overline{XC_m}}$$

where $\{NA_m(k)\}$ is said first data set of said processed experiment profile PA_m, and $\{NC_m(k)\}$ is said second data set of said processed reference profile PC_m; where $\overline{XA_m}$ is an average of measurements, ~~error-model based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents of said data set $\{XA_m(k)\}$, and $\overline{XC_m}$ is an average of measurements, ~~error-model based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents of data set $\{XC_m(k)\}$; and wherein $\overline{XAC}$ is an average calculated according to the equation

$$\overline{XAC} = \frac{1}{2M} \sum_{m=1}^{M} (\overline{XA_m} + \overline{XC_m}).$$

102. (Previously Presented) The computer program product of claim 101, wherein the method further comprises normalizing errors of said experiment profile XA_m and reference profile XC_m according to the equations:

$$\sigma_m^A(k) = \frac{\sigma_m^{XA}(k) - \overline{XAC}}{\overline{XA_m}}$$

and

$$\sigma_m^C(k) = \frac{\sigma_m^{XC}(k) - \overline{XAC}}{\overline{XC_m}}$$

where $\sigma_m^{XA}(k)$ and $\sigma_m^{XC}(k)$ are the standard errors of $XA_m(k)$ and $XC_m(k)$,

respectively, and $\sigma_m^A(k)$ and $\sigma_m^C(k)$ are normalized standard errors of $NA_m(k)$ and $NC_m(k)$, respectively.

103. (Previously Presented) The computer program product of claim 102, wherein the method further comprises normalizing background errors of said experiment profile XA_m and reference profile XC_m according to the equations:

$$bkgstd_m^A(k) = \frac{bkgstd_m^{XA}(k)\overline{XA_m}}{\overline{XA_m}}$$

and

$$bkgstd_m^C(k) = \frac{bkgstd_m^{XC}(k)\overline{XAc}}{\overline{XC_m}}$$

where $bkgstd_m^{XA}(k)$ and $bkgstd_m^{XC}(k)$ are the standard background errors of $XA_m(k)$ and $XC_m(k)$, respectively, and $bkgstd_m^A(k)$ and $bkgstd_m^C(k)$ are normalized standard background errors of said $NA_m(k)$ and said $NC_m(k)$, respectively.

104. (**Currently Amended**) The computer program product of claim 102, wherein the method further comprises determining said averages $\overline{XA_m}$ and $\overline{XC_m}$ excluding measurements of said plurality of different cellular constituents having a value among the highest 10% of said measurements~~, error-model based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of

different cellular constituents in said data sets $\{XA_m(k)\}$ and $\{XC_m(k)\}$, respectively.

105. (Previously Presented) The computer program product of claim 99, wherein said processing step (a) comprises:

normalizing each said experiment profile XA_m and reference profile XC_m to generate normalized data set $\{NA_m(k)\}$ and normalized data set $\{NC_m(k)\}$, respectively;

transforming said normalized data set $\{NA_m(k)\}$ to obtain a transformed data set $\{TA_m(k)\}$, where said transformed data set $\{TA_m(k)\}$ is said first data set of said processed experiment profile PA_m; and

transforming said normalized data set $\{NC_m(k)\}$ to obtain a transformed data set $\{TC_m(k)\}$, where said transformed data set $\{TC_m(k)\}$ is said second data set of said processed reference profile PC_m;

wherein said transforming is carried out for an experiment according to equations

$$TA_m(k) = f(x) = \frac{\ln\left[\frac{b^2+2\cdot a^2\cdot NA_m(k)+2\cdot\sqrt{b^2+b^2\cdot aNA_m(k)+a^2\cdot[aNA_m(k)]^2}}{a}\right]}{a} + d,$$

for $NA_m(k)>0$

and

$$TC_m(k) = f(x) = \frac{\ln\left[\frac{b^2+2\cdot a^2\cdot NC_m(k)+2\sqrt{b^2+b^2\cdot aC_m(k)+a^2\cdot[aC_m(k)]^2}}{a}\right]}{a} + d,$$

for $NC_m(k)>0$

where d is described by equation

$$d = \frac{\ln\left[\frac{b^2}{a}+2\cdot a\right]}{a}$$

and where a is the fractional error coefficient of said experiment, b is the Poisson error coefficient of said experiment, and c is the standard deviation of background noise of said experiment.

106. (Canceled)

107. (Previously Presented) The computer program product of claim 99, wherein said processing step (a) comprises:

normalizing each said experiment profile XA_m and reference profile XC_m to generate normalized data set $\{NA_m(k)\}$ and normalized data set $\{NC_m(k)\}$, respectively;

transforming said normalized data set $\{NA_m(k)\}$ to a new domain in which variance becomes a constant to obtain a transformed data set $\{TA_m(k)\}$;

transforming said normalized data set $\{NC_m(k)\}$ to a new domain in which variance becomes a constant to obtain a transformed data set $\{TC_m(k)\}$; and

removing nonlinearity from each said transformed data sets $\{TA_m(k)\}$ and $\{TC_m(k)\}$, respectively.

108. (Previously Presented) The computer program product of claim 107, wherein said removing nonlinearity is carried out by a method comprising

(a1) calculating an average transformed profile of transformed experiment profiles and transformed reference profiles, wherein each of said transformed

experiment profiles contains a corresponding said transformed data set $\{TA_m(k)\}$, and each of said transformed reference profiles contains a corresponding said transformed data set $\{TC_m(k)\}$; and

(a2) calculating first differences between each of said transformed experiment profiles and said average transformed profile; calculating second differences between each of said transformed reference profiles and said average transformed profile; adjusting, wherein the adjusting comprises correcting nonlinearity each of said transformed experiment profiles based on said first differences between each of said transformed experiment profiles and said average transformed profile, and adjusting, wherein the adjusting comprises correcting nonlinearity each of said transformed reference profiles based on said second differences between each of said transformed reference profiles and said average transformed profile.

109. (**Currently Amended**) The computer program product of claim 108, wherein the method further comprises calculating said first differences based on the differences in a first subset of ~~**error model based transformed measurements or logarithm based**~~ transformed measurements of said plurality of different cellular constituents between each of said transformed experiment profiles and said average transformed profile, and calculating said second differences based on the differences in a second subset of ~~**error model based transformed measurements or logarithm based**~~ transformed measurements of said plurality of different cellular constituents

between each of said transformed reference profiles and said average transformed profile.

110. (**Currently Amended**) The computer program product of claim 109, wherein each said first subset consists of ~~**error-model-based transformed measurements or logarithm-based**~~ transformed measurements that are ranked similarly between each of said transformed experiment profiles and said average transformed profile, and each said second subset consists of ~~**error-model-based transformed measurements or logarithm-based**~~ transformed measurements that are ranked similarly between each of said transformed reference profiles and said average transformed profile.

111. (**Currently Amended**) The computer program product of claim 110, wherein said adjusting step (a2) is carried out by a method comprising:

(a2l) binning said first subset into a plurality of bins, each said bin consisting of ~~**error-model-based transformed measurements or logarithm-based**~~ transformed measurements of said plurality of different cellular constituents in one of said transformed experiment profiles and said average transformed profile having a value in a given range; and binning said second subset into a plurality of bins, each said bin consisting of **error-model-based** ~~**transformed measurements or logarithm-based**~~ transformed measurements of said plurality of different cellular constituents in one of said transformed reference profiles and said average transformed profile having a value in a given range;

and computing corrected ~~error-model-based transformed measurements or logarithm-based~~ transformed measurements of said plurality of different cellular constituents in each said transformed data set $\{TC_m(k)\}$, according to the equation:

$$TC_m^{corr}(k) = TC_m(k) - nonlinear\_TC_m(k),$$

where k = 1, ..., N; and where $\{TA_m^{corr}(k)\}$ is said first processed data set of said processed experiment profile PA_m, and $\{TC_m^{corr}(k)\}$ is said second processed data set of said processed reference profile PC_m.

112. (**Currently Amended**) The computer program product of claim 111, wherein said processed experiment profile PA_m and said processed reference profile PC_m comprise ~~error model based transformed measurements or logarithm based~~ transformed measurements of said plurality of different cellular constituents from the same experimental reaction.

113. (**Currently Amended**) The computer program product of claim 112, wherein the method further comprises calculating $\overline{PC}(k)$ according to the equation

$$\overline{PC}(k) = \frac{1}{M}\sum_{m=1}^{M} PC_m(k),$$

wherein $\{PC_m(k)\}$ comprises ~~error-model-based transformed measurements or logarithm-based~~ transformed measurements from said second processed data set $\{TC_m^{corr}(k)\}$ and calculating said differential reference profile according to the

equation

$$PC_{diff}(m,k) = PC_m(k) - \overline{PC}(k)$$

and wherein said first error-corrected profile is calculated according to the equation

$$PA'_m(k) = PA_m(k) - PC_{diff}(m,k),$$

wherein $\{PA_m(k)\}$comprises ~~error-model-based transformed measurements or logarithm-based~~ transformed measurements from said first data set $\{TA^{corr}_m(k)\}$.

114. (Previously Presented) The computer program product of claim 113, wherein the method further comprises

(d) calculating for each processed profile pair $\{PA_m, PC_m\}$, where m $\in\{1, 2, ..., M\}$, a second error-corrected experiment profile PA''_m comprising data set $\{PA''_m(k)\}$ by combining said first error-corrected experiment profile PA'_m with said processed experiment profile PA_m using a weighing factor {w(k)}, k = 1,2, ..., N, wherein w(k) is a weighing factor for the k'th measurement.

115. (Previously Presented) The computer program product of claim 114, wherein said second error-corrected experiment profile PA''_m is calculated according to the equation

$$PA''_m(k) = (1\text{-}w(k)) \cdot PA_m(k) + w(k)PA'_m(k).$$

116. (Previously Presented) The computer program product of claim 115, wherein the method further comprises determining said weighing factor according to

the equation

$$w(k) = 1 - e^{-0.5\left[\frac{PC(k)}{avg\_bkgstd}\right]^2}$$

where *avg_bkgstd* is an average background standard error.

117. (Previously Presented) The computer program product of claim 116, wherein the method further comprises determining said *avg_ bkgstd* according to the equation

$$avg\_bkgstd = \frac{1}{N}\sum_{k=1}^{N}\left[\frac{1}{M}\sum_{m=1}^{M} bkgstd(m,k)\right]$$

where *bkgstd (m, k)* is background standard error of $PC_m(k)$.

118. (Previously Presented) The computer program product of claim 113, wherein the method further comprises determining errors $\{P\sigma'_m\}$ of said first error-corrected experiment profile $\{PA'_m\}$, wherein said $\{P\sigma'_m\}$ comprises error data set $\{P\sigma'_m(k)\}$.

119. (Previously Presented) The computer program product of claim 118, wherein the method further comprises determining said error data set $\{P\sigma'_m(k)\}$ according to the equation

$$\sigma'_m(k) = \sqrt{P\sigma_m^2(k) + mixed\_P\sigma_m^2(k) - 2Cor(k)\cdot P\sigma_m(k)\cdot mixed\_P\sigma_m(k)}$$

where $P\sigma_m(k)$ is the standard error of $A_m(k)$, and determining $mixed\_P\sigma_m(k)$

according to the equation

$$mixed\_P\sigma_m(k) = \frac{P\sigma_m(k) + (M-1)P\sigma_{pool}(k)}{M}$$

where

$$P\sigma_{pool}(k) = \sqrt{\frac{1}{M-1}\sum_{m}^{M}(PC_m(k) - \overline{PC}(k))^2}$$

and where Cor(k) is a correlation coefficient between said processed experiment profile PA_m and said processed reference profile PC_m.

120. (Previously Presented) The computer program product of claim 119, wherein said Cor(k) is determined according to the equation

$$Cor(k) = CorMax \cdot \left[1 - e^{-0.5\left[\frac{PC(k)}{\sigma_{mix}(k)}\right]^2}\right]$$

where CorMax is a number between 0 and 1.

121. (Previously Presented) The computer program product of claim 120, wherein the method further comprises determining errors $\{P\sigma''_m\}$ of said second error-corrected experiment profile $\{PA''_m\}$ wherein said $\{P\sigma''_m\}$ comprises error data set $\{P\sigma''_m(k)\}$.

122. (Previously Presented) The computer program product of claim 121, wherein the method further comprises determining said error data set $\{P\sigma''_m(k)\}$ according to the equation

$$P\sigma^{*}_{m}(k) = \sqrt{[1 - w(k)] \cdot P\sigma^{2}_{m}(k) + w(k) P\sigma'^{2}_{m}(k)}$$

where $P\sigma_{m}(k)$ is the standard error of $PA_{m}(k)$, and the method further comprises determining $P\sigma'_{m}(k)$ according to the equation

$$P\sigma'_{m}(k) = \sqrt{P\sigma^{2}_{m}(k) + mixed\_P\sigma_{m}{}^{2}(k) - 2 \cdot Cor(k) \cdot P\sigma_{m}(k) \cdot mixed\_P\sigma_{m}(k)},$$

and

the method further comprises determining $mixed\_P\sigma_{m}(k)$ according to the equation

$$mixed\_P\sigma_{m}(k) = \frac{P\sigma_{m}(k) + (M-1) \cdot P\sigma_{ref}(k)}{M}$$

where

$$P\sigma_{ref}(k) = \sqrt{\frac{1}{M-1} \sum_{m}^{M} (PC_{m}(k) - PC(k))^{2}}$$

and where Cor(k) is a correlation coefficient between said processed experiment profile PA_{m} and said processed reference profile PC_{m}.

123. (Previously Presented) The computer program product of claim 122, wherein the method further comprises determining said Cor(k) according to the equation

$$Cor(k) = CorMax \cdot \left[1 - e^{-0.5\left[\frac{\overline{PC(k)}}{avg.sigma}\right]^{2}}\right]$$

where CorMax is a number between 0 and 1.

124. (Previously Presented) The computer program product of claim 123, wherein each said pair of profiles XA_m and XC_m comprise measurements of said plurality of different cellular constituents from a two-channel microarray experiment.

125. (Previously Presented) The computer program product of claim 124, wherein said reference profiles $\{XC_m\}$, m = 1, 2, ... , M, are measured with samples labeled with a same label.

126. (Previously Presented) The computer program product of claim 125, wherein at least one of said pairs of profiles $\{XA_m, XC_m\}$ is a virtual profile.

127. (**Currently Amended**) A computer program product for use in conjunction with a computer having a processor and a memory connected to the processor, said computer program product comprising a computer readable storage medium having a computer program mechanism encoded thereon, wherein said computer program mechanism may be loaded into the memory of said computer and cause said computer to carry out a method for generating at least one error-corrected experiment profile of at least one experiment profile A_m, where m $\in$ {1, 2, ..., M} in at least one of a plurality of pairs of profiles $\{A_m, C_m\}$, A_m being an experiment profile, C_m being a reference profile, where m = 1, 2, ... , M, M is the number of pairs of profiles, said method comprising:

via ~~said~~ a differential reference profile $C_{diff}(m,k)$ calculated between C_m and an average reference profile $\bar{C}$ determined for profile pair $\{A_m, C_m\}$ where $m \in \{1, 2, ..., M\}$, wherein said average reference profile $\bar{C}$ comprises data set $\{\bar{C}(k)\}$, removing, on a computer, systematic cross-experiment error from said experiment profile A_m to generate a first error-corrected experiment profile A'_m; wherein said average reference profile $\bar{C}$ is an average of reference profiles $\{C_m\}$, $m = 1, 2, ..., M$; wherein for each $m \in \{1, 2, ..., M\}$, said first error-corrected experiment profile A'_m comprises data set $\{A'_m(k)\}$, said experiment profile A_m comprises data set $\{A_m(k)\}$, and said reference profile C_m comprises data set $\{C_m(k)\}$, ~~and said average reference profile $\bar{C}$ comprises data set $\{\bar{C}(k)\}$,~~ wherein said data set $\{A_m(k)\}$ comprises measurements~~, error-model-based transformed measurements, or logarithm-based transformed measurements~~ of a plurality of different cellular constituents measured in a sample having been subject to a first condition, said data set $\{C_m(k)\}$ comprises measurements~~, error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents measured in a sample having been subject to a second condition, wherein $k = 1, 2, ..., N$; k is an index of measurements~~, error-model-based transformed measurements, or logarithm-based transformed measurements~~ of cellular constituents, N being the total number of measurements, wherein generating respective $A'_m(k)$ of said first error-corrected experiment profile A'_m comprises subtracting $C_{diff}(m,k)$ from $A_m(k)$;

~~obtaining a data set $\{A''_m(k)\}$, wherein obtaining said data set $\{A''_m(k)\}$ comprises combining said first error-corrected experiment profile A'_m with said experiment profile A_m using a weighing factor $\{w(k)\}$, $k = 1, 2, \ldots, N$, wherein $w(k)$ is a weighing factor for a k'th measurement;~~ and

outputting to a user, a user interface device, a computer readable storage medium, or a local or remote computer system; or displaying: said first error-corrected experiment profile A'_m[[,]] or said data set $\{A'_m(k)\}$, ~~a second error-corrected experiment profile A''_m, or said data set $\{A''_m(k)\}$, wherein said second error-corrected experiment profile A''_m comprises said data set $\{A''_m(k)\}$~~.

128. (Previously Presented) The computer program product of claim 88, wherein the method further comprises obtaining said transformed measurements of said data set $\{A_m(k)\}$ and said data set $\{C_m(k)\}$ for an experiment according to the equations:

$$A_m(k) = f(x) = \frac{\ln\left[\frac{b^2+2\cdot a^2\cdot XA_m(k)}{a}+2\sqrt{c^2+b^2\cdot XA_m(k)+a^2\cdot[XA_m(k)]^2}\right]}{a}+d,$$

for $XA_m(k)>0$

and

$$C_m(k) = f(x) = \frac{\ln\left[\frac{b^2+2\cdot a^2\cdot XC_m(k)}{a}+2\sqrt{c^2+b^2\cdot XC_m(k)+a^2\cdot[XC_m(k)]^2}\right]}{a}+d,$$

for $XC_m(k)>0$

where $\{XA_m(k)\}$ and $\{XC_m(k)\}$ are data sets comprising measurements of said plurality of different cellular constituents that when transformed produce said transformed measurements of said plurality of different cellular constituents of said data set $A_m(k)$ and said data set $C_m(k)$, respectively, where d is described by the equation:

$$d = \frac{-a_m\left[\frac{b^2}{a} + 3 \cdot c\right]}{a}$$

and where a is the fractional error coefficient of said experiment, b is the Poisson error coefficient of said experiment, and c is the standard deviation of background noise of said experiment.

129. (Previously Presented) The computer program product of claim 99, wherein said processing comprises:

normalizing, transforming, and/or removing nonlinearity from measurements of said plurality of cellular constituents of said data set $\{XA_m(k)\}$ of said experiment profile XA_m, and from measurements of said plurality of cellular constituents of said data set $\{XC_m(k)\}$ of said reference profile XC_m.

130. **(Currently Amended)** A computer system comprising:

a processor; and

a memory coupled to said processor and encoding one or more programs;

wherein said one or more programs cause the processor to carry out a method for generating at least one error-corrected experiment profile of at least one experiment profile in a plurality of pairs of profiles $\{A_m,C_m\}$, where m = 1, 2, …, M, and M is the number of the pairs of profiles; and wherein, for each m ∈ {1, 2, …, M}, A_m is an experiment profile, and C_m is a reference profile; and wherein $\{A_m\}$ represents experiment profiles in said plurality of pairs of profiles $\{A_m,C_m\}$ and $\{C_m\}$ represents reference profiles in said plurality of pairs of profiles $\{A_m, C_m\}$, said method comprising:

(a) calculating, on a computer, an average reference profile $\bar{C}$ of said plurality of reference profiles $\{C_m\}$ where m = 1, 2, …, M;

(b) determining, on a computer, for at least one profile pair $\{A_m,C_m\}$where m ∈ {1, 2, …, M} of said plurality of pairs of profiles $\{A_m, C_m\}$ a differential reference profile $C_{diff}(m, k)$ computed between C_m and $\bar{C}$, **wherein said average reference profile $\bar{C}$ comprises data set $\{\bar{C}(k)\}$**;

(c) via said differential reference profile determined for said profile pair, removing, on a computer, systematic cross-experiment error from an experiment profile A_m of said at least one profile pair $\{A_m, C_m\}$ where m ∈ {1, 2, …, M} to generate a first error-corrected experiment profile A'_m for each m ∈ {1, 2, …, M}, wherein said experiment profile A_m comprises a first data set$\{A_m(k)\}$, said reference profile C_m comprises a second data set, ~~said average reference profile $\bar{C}$ comprises data set $\{\bar{C}(k)\}$,~~ and said first error-corrected experiment profile A'_m comprises data set $\{A'_m(k)\}$;

wherein said first data set comprises measurements~~, error-model-based transformed measurements, or logarithm-based transformed measurements~~ of a plurality of different cellular constituents measured in a sample having been subject to a first condition, said second data set comprises measurements~~, error-model based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents measured in a sample having been subject to a second condition; and wherein k = 1, 2, ..., N; k is an index of measurements~~, error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents, N being the total number of measurements~~, error-model-based transformed measurements, or logarithm-based transformed measurements~~, wherein said first error-corrected experiment profile A'_m is generated according to the equation

$A'_m(k) = A_m(k) - C_{drift}(m,k)$; and

~~(d) obtaining a data set $\{A''_m(k)\}$, wherein obtaining said data set $\{A''_m(k)\}$ comprises combining said first error-corrected experiment profile A'_m with said experiment profile A_m using a weighing factor $\{w(k)\}$, k = 1, 2, ..., N, wherein $w(k)$ is a weighing factor for a k^{th} measurement; and~~

~~(e)~~ (d) outputting to a user, a user interface device, a computer readable storage medium, or a local or remote computer system; or displaying; said first error-corrected experiment profile $A'_m[[,]]$ or said data set $\{A'_m(k)\}$~~, a second error-corrected experiment profile A''_m, or said data set $\{A''_m(k)\}$, wherein said second error-~~

~~corrected experiment profile A''_m comprises said data set $\{A''_m(k)\}$.~~

131. (Previously Presented) The computer system of claim 130, wherein said steps (b) and (c) are performed for each profile pair $\{A_m, C_m\}$ where $m \in \{1, 2, \ldots, M\}$.

132. **(Currently Amended)** The computer system of claim 131, wherein each of said experiment profile A_m and said reference profile C_m comprises measurements~~, error-model-based-transformed-measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents from the same experimental reaction.

133. (Previously Presented) The computer system of claim 132, wherein said $\bar{C}(k)$ is calculated according to the equation

$$\bar{C}(k) = \frac{1}{M}\sum_{m=1}^{M} C_m(k)$$

Wherein said differential reference profile is determined according to the equation

$$C_{diff}(m,k) = C_m(k) - \bar{C}(k)$$

and wherein said first error-corrected experiment profile A'_m is generated according to the equation

$$A'_m(k) = A_m(k) - C_{m,f}(m,k)$$

wherein $\{A_m(k)\}$ is said first data set of experiment profile A_m.

134. (**Currently Amended**) The computer system of claim 133, wherein the method further comprises:

~~(d)~~ (c) calculating, for one or more remaining profile pairs out of said profile pairs $\{A_m, C_m\}$, a respective second error-corrected experiment profile A''_m; and

~~(e)~~ (f) outputting to, a user interface device, a computer readable storage medium, or a local or remote computer system; or displaying; said respective second error-corrected experiment profile A''_m or ~~said~~ a data set $\{A''_m(k)\}$.

135. (Previously Presented) The computer system of claim 134, wherein said second error-corrected experiment profile A''_m is calculated according to the equation

$$A''_m(k) = (1-w(k)) \cdot A_m(k) + w(k) \cdot A'_m(k).$$

136. (**Currently Amended**) The computer system of claim 135, wherein the method further comprises determining ~~said~~ a weighing factor $w(k)$ according to the equation

$$w(k) = 1 - e^{-0.5\left[\frac{2(k)}{\text{avg\_diagonal}}\right]^2}$$

where *avg_bkgstd* is an average background standard error.

137. (Previously Presented) The computer system of claim 136, wherein the method further comprises determining said *avg_bkgstd* according to the equation

$$avg\_bkgstd = \frac{1}{N}\sum_{k=1}^{N}\left[\frac{1}{M}\sum_{m=1}^{M} bkgstd(m,k)\right]$$

where *bkgstd (m, k)* is background standard error of $C_m(k)$.

138. (Previously Presented) The computer system of claim 133, wherein the method further comprises determining errors $\{\sigma'_m(k)\}$ of said data set $\{A'_m(k)\}$ in said first error-corrected experiment profile A'_m.

139. (Previously Presented) The computer system of claim 138, wherein the method further comprises determining said errors $\{\sigma'_m(k)\}$ according to the equation

$$\sigma'_m(k) = \sqrt{\sigma_m^2(k) + mixed\_\sigma_m^2(k) - 2 \cdot Cor(k) \cdot \sigma_m(k) \cdot mixed\_\sigma_m(k)}$$

where $\sigma_m(k)$ is the standard error of $A_m(k)$, the method further comprising determining $mixed\_\sigma_m(k)$ according to the equation

$$mixed\_\sigma_m(k) = \frac{\sigma_m(k) + (N-1)\sigma_{ref}(k)}{N}$$

where $\sigma_{ref}(k) = \sqrt{\frac{1}{N-1}\sum_{m}^{M}(C_m(k) - \bar{C}(k))^2}$

and where Cor(k) is a correlation coefficient between said experiment profile A_m and said reference profile C_m.

140. (Previously Presented) The computer system of claim 139, wherein the method further comprises determining said Cor(k) according to the equation

$$Cor(k) = CorMax \cdot \left[1 - e^{-0.5 \cdot \left[\frac{\bar{c}(k)}{\sigma_{background}}\right]^2}\right]$$

where CorMax is a number between 0 and 1.

141. (Previously Presented) The computer system of claim 136, wherein the method further comprises determining errors $\{\sigma''_m(k)\}$ of said data set $\{A''_m(k)\}$ in said second error-corrected experiment profile A''_m.

142. (Previously Presented) The computer system of claim 141, wherein said errors $\{\sigma''_m(k)\}$ are determined according to the equation

$$\sigma''_m(k) = \sqrt{[1 - w(k)] \cdot \sigma_m^2(k) + w(k)\sigma'^2_m(k)}$$

where $\sigma_m(k)$ is the standard error of $A_m(k)$, the method further comprising (i) determining $\sigma'_m(k)$ according to the equation

$$\sigma'_m(k) = \sqrt{\sigma_m^2(k) + mixed\_\sigma_m^2(k) - 2 \cdot Cor(k) \cdot \sigma_m(k) \cdot mixed\_\sigma_m(k)}, \text{ and}$$

(ii) determining $mixed\_\sigma_m(k)$ according to the equation

$$mixed\_\sigma_m(k) = \frac{\sigma_m(k) + (M-1)\cdot\sigma_{ref}(k)}{M}$$

where $\sigma_{ref}(k) = \sqrt{\frac{1}{M-1}\sum_{m}^{M}(c_m(k) - \bar{C}(k))^2}$

and where Cor(k) is a correlation coefficient between said experiment profile A_m and said reference profile C_m.

143. (Previously Presented) The computer system of claim 142, wherein the method further comprises determining said Cor(k) according to the equation

$$Cor(k) = CorMax \cdot \left[1 - e^{-0.5\left[\frac{\bar{C}(k)}{\mathrm{mixed\_std}}\right]^2}\right]$$

where CorMax is a number between 0 and 1.

144. (Previously Presented) The computer system of claim 131, wherein said experiment profile A_m and said reference profile C_m of each said profile pair $\{A_m, C_m\}$ are measured in a two-channel microarray experiment.

145. (Previously Presented) The computer system of claim 144, wherein said reference profiles $\{C_m\}$, where $m = 1, 2, \ldots, M$, are measured with samples labeled with a same label.

146. (Previously Presented) The computer system of claim 131, wherein at least one of said plurality of pairs of profiles $\{A_m, C_m\}$ is a virtual profile.

147. (**Currently Amended**) The computer system of claim 130, wherein said plurality of pairs of profiles $\{A_m, C_m\}$ are transformed profiles each comprising ~~error-model based transformed measurements or logarithm-based~~ transformed measurements of said plurality of different cellular constituents in data set $\{A_m(k)\}$ and data set $\{C_m(k)\}$, respectively; and wherein said data set $\{A_m(k)\}$ is said first data set, and said data set $\{C_m(k)\}$ is said second data set.

148. (**Currently Amended**) The computer system of claim 130, wherein the method further comprises:

(a0) removing nonlinearity, prior to said calculating step (a), from measurements, ~~error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents to generate said plurality of pairs of profiles $\{A_m, C_m\}$ comprising said experiment profile A_m and reference profile C_m.

149. (**Currently Amended**) The computer system of claim 148, wherein said removing step (a0) comprises:

(a0i) calculating an average profile of pre-experiment profiles $\{A_m^{pre}\}$ and pre- reference profiles $\{C_m^{pre}\}$; wherein each of said pre-experiment profiles

comprises measurements~~, error model based transformed measurements, or logarithm based transformed measurements~~ of said plurality of different cellular constituents measured in said sample having been subject to said first condition, which when nonlinearity is removed therefrom, produces each said experiment profile A_m; and wherein each of said pre-reference profiles comprises measurements~~, error model based transformed measurements, or logarithm based transformed measurements~~ of said plurality of different cellular constituents measured in said sample having been subject to said second condition, which when nonlinearity is removed therefrom, produces each said reference profile C_m; and

(a0ii) calculating first differences between each of said pre-experiment profiles $\{A_m^{pre}\}$ and said average profile; calculating second differences between each of said pre-reference profiles $\{C_m^{pre}\}$ and said average profile; adjusting, wherein the adjusting comprises correcting nonlinearity, each of said pre-experiment profiles $\{A_m^{pre}\}$ based on said first differences between each of said pre-experiment profiles $\{A_m^{pre}\}$ and said average profile, thereby generating each said experiment profile A_m; and adjusting, wherein the adjusting comprises correcting nonlinearity, each of pre-reference profiles $\{C_m^{pre}\}$ based on said second differences between each of said pre-reference profiles $\{C_m^{pre}\}$ and said average profile, thereby generating each said reference profile C_m.

150. **(Currently Amended)** The computer system of claim 149, wherein the method further comprises calculating said first differences based on a first subset of said measurements, ~~**error-model-based transformed measurements, or logarithm-based-transformed-measurements**~~ of said plurality of different cellular constituents in said pre-experiment profiles $\{A_m^{pre}\}$ and said average profile; and calculating said second differences based on a second subset of said measurements, ~~**error-model-based transformed measurements, or logarithm-based transformed measurements**~~ of said plurality of different cellular constituents in said pre-reference profiles $\{C_m^{pre}\}$ and said average profile.

151. **(Currently Amended)** The computer system of claim 150, wherein said first subset consists of measurements, ~~**error-model-based transformed measurements, or logarithm-based-transformed-measurements**~~ of said plurality of different cellular constituents that are ranked similarly between each of said pre-experiment profiles $\{A_m^{pre}\}$ and said average profile, and said second subset consists of measurements, ~~**error-model-based transformed measurements, or logarithm-based transformed-measurements**~~ of said plurality of different cellular constituents that are ranked similarly between each of said pre-reference profiles $\{C_m^{pre}\}$ and said average profile.

152. **(Currently Amended)** The computer system of claim 151, wherein

said adjusting step (a0ii) is carried out by a method comprising:

(ii1) binning said first subset into a first plurality of bins, wherein each of said first plurality of bins consists of measurements~~, error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents in one of said pre-experiment profiles $\{A_m^{pre}\}$ and said average profile having a value in a given range; and binning said second subset into a second plurality of bins, wherein each of said second plurality of bins consists of measurements~~, error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents in one of said pre-reference profiles $\{C_m^{pre}\}$ and said average profile having a value in a given range;

(ii2) calculating, in each bin of said first plurality of bins, a first mean difference between a feature value of measurements~~, error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said one of said pre-experiment profiles $\{A_m^{pre}\}$ and a feature value of said average profile, and calculating a second mean difference between a feature value of measurements~~, error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said one of said pre-reference profiles $\{C_m^{pre}\}$ and a feature value of said average profile;

(ii3) determining a first curve of said first mean difference as a first function of values of measurements~~, error-model-based transformed measurements, or~~

~~logarithm-based transformed measurements~~ of said plurality of different cellular constituents for said one of said pre-experiment profiles $\{A_m^{pre}\}$, wherein said first function is represented by, $nonlinear\_A_m^{pre}$; and determining a second curve of said second mean difference as a second function of values of measurements, ~~error-model based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents for said one of said pre-reference profiles $\{C_m^{pre}\}$, wherein said second function is represented by $nonlinear\_C_m^{pre}$; and

(ii4) adjusting each of said pre-experiment profiles $\{A_m^{pre}\}$ according to the equation:

$$A_m(k) = A_m^{pre}(k) - nonlinear\_A_m^{pre}(k),$$

and adjusting each of said pre-reference profiles $\{C_m^{pre}\}$ according to the equation:

$$C_m(k) = C_m^{pre}(k) - nonlinear\_C_m^{pre}(k),$$

where k = 1, ... , N; and where $A_m^{pre}(k)$ and $C_m^{pre}(k)$ are data sets of each of said pre-experiment profiles $\{A_m^{pre}\}$ and each of said pre-reference profiles $\{C_m^{pre}\}$, respectively; and where $A_m(k)$ and $C_m(k)$ are said first data set and said second data set, respectively.

153. **(Currently Amended)** The computer system of claim 130, wherein

the method further comprises:

(a0) normalizing, prior to said calculating step (a), measurements~~, error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents in a pre-experiment profile A_m^{pre} and a pre-reference profile C_m^{pre} to generate said experiment profile A_m and said reference profile C_m, respectively.

154. (**Currently Amended**) The computer system of claim 153, wherein said normalizing step (a0) comprises normalizing a data set $A_m^{pre}(k)$ and a data set $C_m^{pre}(k)$, according to the equations:

$$A_m(k) = \frac{A_m^{pre}(k)\,\overline{A_m^{pre}}\,\overline{C_m^{pre}}}{\overline{A_m^{pre}}}$$

and

$$C_m(k) = \frac{C_m^{pre}(k)\,\overline{A_m^{pre}}\,\overline{C_m^{pre}}}{\overline{C_m^{pre}}},$$

wherein said data sets $A_m^{pre}(k)$ and $C_m^{pre}(k)$ each comprises measurements~~, error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents, where $\overline{A_m^{pre}}$ is an average of measurements~~, error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents in said $A_m^{pre}(k)$, and $\overline{C_m^{pre}}$ is an average of measurements~~, error-model-~~

~~based transformed measurements, or logarithm based transformed measurements~~ of said plurality of different cellular constituents in said $C_m^{pre}(k)$, wherein $A_m(k)$ is said first data set, wherein $A_m(k)$ comprises normalized measurements ~~or normalized error model based transformed measurements, or normalized logarithm based transformed measurements~~ of said pre-experiment profile A_m^{pre}; and $C_m(k)$ is said second data set wherein $A_m(k)$ comprises normalized measurements ~~or normalized error model based transformed measurements, or normalized logarithm based transformed measurements~~ of said reference profile C_m^{pre}; and wherein $\overline{A_m^{pre} C_m^{pre}}$ is an average calculated according to the equation

$$\overline{A_m^{pre} C_m^{pre}} = \frac{1}{2M} \sum_{m=1}^{M} \overline{(A_m^{pre} + C_m^{pre})}.$$

155. (Previously Presented) The computer system of claim 154, wherein the method further comprises normalizing errors of said data sets $\{ A_m^{pre}(k) \}$ and $\{ C_m^{pre}(k) \}$, respectively, according to the equations:

$$\sigma_m^{NA}(k) = \frac{\sigma_m^{proA}(k) \overline{A_m^{pre} C_m^{pre}}}{A_m^{pre}}$$

and

$$\sigma_m^{NC}(k) = \frac{\sigma_m^{proC}(k) \overline{A_m^{pre} C_m^{pre}}}{C_m^{pre}},$$

where $\sigma_m^{preA}(k)$ and $\sigma_m^{preC}(k)$ are the standard errors of $A_m^{pre}(k)$ and $C_m^{pre}(k)$, respectively, and $\sigma_m^{NA}(k)$ and $\sigma_m^{NC}(k)$ are normalized standard errors of $A_m(k)$ and $C_m(k)$, respectively.

156. (Previously Presented) The computer system of claim 155, wherein the method further comprises normalizing background errors of said data sets $\{A_m^{pre}(k)\}$ and $\{C_m^{pre}(k)\}$, respectively, according to the equations:

$$bkgstd_m^{NA}(k) = \frac{bkgstd_m^{preA}(k)\overline{A_m^{pre}C_m^{pre}}}{\overline{A_m^{pre}}}$$

and

$$bkgstd_m^{NC}(k) = \frac{bkgstd_m^{preC}(k)\overline{A_m^{pre}C_m^{pre}}}{\overline{C_m^{pre}}}$$

where $bkgstd_m^{preA}(k)$ and $bkgstd_m^{preC}(k)$ are the standard background errors of $A_m^{pre}(k)$ and $C_m^{pre}(k)$, respectively, and $bkgstd_m^{NA}(k)$ and $bkgstd_m^{NC}(k)$ are normalized standard background errors of $A_m(k)$ and $C_m(k)$, respectively.

157. (**Currently Amended**) The computer system of claim 156, wherein the method further comprises calculating said averages $\overline{A_m^{pre}}$ and $\overline{C_m^{pre}}$ by excluding measurements~~, error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents having

a value among the highest 10% of said measurements, ~~error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents in said data sets $\{A_m^{pre}(k)\}$ and $\{C_m^{pre}(k)\}$, respectively.

158. **(Currently Amended)** A computer system comprising:

a processor; and

a memory coupled to said processor and encoding one or more programs; wherein said one or more programs cause the processor to carry out a method for generating at least one error-corrected experiment profile of at least one experiment profile in a plurality of pairs of profiles $\{XA_m, XC_m\}$, XA_m being an experiment profile, XC_m being a reference profile, where m = 1, 2, ... , M, M is the number of pairs of profiles, said method comprising:

(a) processing, on a computer, said plurality of pairs of profiles $\{XA_m, XC_m\}$ to obtain a plurality of pairs of processed profiles $\{PA_m, PC_m\}$, PA_m being a processed experiment profile, PC_m being a processed reference profile, wherein said processing comprises normalizing at least one said experiment profile XA_m and reference profile XC_m;

(b) calculating, on a computer, an average processed reference profile $\overline{PC}$ of processed reference profiles $\{PC_m\}$, where m = 1,2, ..., M;

(c) determining, on a computer, for at least one processed profile pair $\{PA_m$,

PC_m} where m ∈ {1, 2, ..., M} of said plurality of pairs of processed profiles {PA_m, PC_m}, where m = 1, 2, ..., M, a differential reference profile **$PC_{diff}(m,k)$** computed between PC_m and $\overline{PC}$ **wherein said average processed reference profile $\overline{PC}$ comprises data set {$\overline{PC}$(k)}**;

(d) via said differential reference profile determined for said at least one processed profile pair, removing, on a computer, systematic cross-experiment error from a processed experiment profile PA_m of said at least one processed profile pair {PA_m, PC_m} where m ∈ {1, 2, ..., M} to generate a first error-corrected processed experiment profile PA'_m ; wherein for each m ∈ {1, 2, ..., M}, said processed experiment profile PA_m comprises a first processed data set **{PA_m(k)}**, said processed reference profile PC_m comprises a second processed data set, ~~said average processed reference profile $\overline{PC}$ comprises data set {$\overline{PC}$(k)}~~, said first error-corrected processed experiment profile PA'_m comprises dataset {PA'_m(k)}, said experiment profile XA_m comprises data set {XA_m(k)}, said reference profile XC_m comprises data set {XC_m(k)}, wherein said data set {XA_m(k)} comprises measurements of a plurality of different cellular constituents measured in a sample having been subject to a first condition, said data set {XC_m(k)} comprises measurements of said plurality of different cellular constituents measured in a sample having been subject to a second condition, and where k = 1, 2, ..., N; k is an index of measurements of cellular constituents, N being the total number of measurements, **wherein said first error-corrected processed experiment profile**

PA'_m is generated according to the equation $PA'_m(k) = PA_m(k) - PC_{mn}(m,k)$; and

~~(e) obtaining data set $\{PA''_m(k)\}$, wherein obtaining said data set $\{PA''_m(k)\}$, comprises combining said first error-corrected processed experiment profile PA'_m with said processed experiment profile PA_m using a weighing factor $\{w(k)\}$, $k = 1, 2, ..., N$, wherein $w(k)$ is a weighing factor for a k'th measurement; and~~

~~(f)~~ (e) outputting to a user, a user interface device, a computer readable storage medium, or a local or remote computer system; or displaying: said first error-corrected processed experiment profile PA'_m [[,]] or said data set $\{PA'_m(k)\}$ ~~a second error-corrected processed experiment profile PA''_m, or said data set $\{PA''_m(k)\}$, wherein said second error-corrected processed experiment profile PA''_m comprises said data set $\{PA''_m(k)\}$~~.

159. (Previously Presented) The computer system of claim 158, wherein said processing step (a) comprises normalizing each said experiment profile XA_m and reference profile XC_m.

160. (**Currently Amended**) The computer system of claim 159, wherein said normalizing is carried out according to the equations:

$$NA_m(k) = \frac{XA_m(k) \cdot \overline{XC}}{\overline{XA_m}}$$

and

$$NC_m(k) = \frac{XC_m(k) \cdot \overline{XAC}}{\overline{XC_m}}$$

where $\{NA_m(k)\}$ is said first data set of said processed experiment profile PA_m, and $\{NC_m(k)\}$ is said second data set of said processed reference profile PC_m; where $\overline{XA_m}$ is an average of measurements, ~~error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents of said data set $\{XA_m(k)\}$, and $\overline{XC_m}$ is an average of measurements, ~~error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular constituents of data set $\{XC_m(k)\}$; and wherein $\overline{XAC}$ is an average calculated according to the equation

$$\overline{XAC} = \frac{1}{2M} \sum_{m=1}^{M} (\overline{XA_m} + \overline{XC_m}).$$

161. (Previously Presented) The computer system of claim 160, wherein the method further comprises normalizing errors of said experiment profile XA_m and reference profile XC_m according to the equations:

$$\sigma_m^A(k) = \frac{\sigma_m^{XA}(k) \cdot \overline{XAC}}{\overline{XA_m}}$$

and

$$\sigma_m^C(k) = \frac{\sigma_m^{XC}(k) \cdot \overline{XAC}}{\overline{XC_m}}$$

where $\sigma_m^{XA}(k)$ and $\sigma_m^{XC}(k)$ are the standard errors of $XA_m(k)$ and $XC_m(k)$,

respectively, and $\sigma_m^A(k)$ and $\sigma_m^C(k)$ are normalized standard errors of $NA_m(k)$ and $NC_m(k)$, respectively.

162. (Previously Presented) The computer system of claim 161, wherein the method further comprises normalizing background errors of said experiment profile XA_m and reference profile XC_m according to the equations:

$$bkgstd_m^A(k) = \frac{bkgstd_m^{XA}(k)\cdot\overline{XA_m}}{\overline{XA_m}}$$

and

$$bkgstd_m^C(k) = \frac{bkgstd_m^{XC}(k)\cdot\overline{XA_m}}{\overline{XC_m}}$$

where $bkgstd_m^{XA}(k)$ and $bkgstd_m^{XC}(k)$ are the standard background errors of $XA_m(k)$ and $XC_m(k)$, respectively, and $bkgstd_m^A(k)$ and $bkgstd_m^C(k)$ are normalized standard background errors of said $NA_m(k)$ and said $NC_m(k)$, respectively.

163. (**Currently Amended**) The computer system of claim 161, wherein the method further comprises determining said averages $\overline{XA_m}$ and $\overline{XC_m}$ excluding measurements of said plurality of different cellular constituents having a value among the highest 10% of said measurements~~, error-model-based transformed measurements, or logarithm-based transformed measurements~~ of said plurality of different cellular

constituents in said data sets $\{XA_m(k)\}$ and $\{XC_m(k)\}$, respectively.

164. (Previously Presented) The computer system of claim 158, wherein said processing step (a) comprises:

normalizing each said experiment profile XA_m and reference profile XC_m to generate normalized data set $\{NA_m(k)\}$ and normalized data set $\{NC_m(k)\}$, respectively;

transforming said normalized data set $\{NA_m(k)\}$ to obtain a transformed data set $\{TA_m(k)\}$, where said transformed data set $\{TA_m(k)\}$ is said first data set of said processed experiment profile PA_m; and

transforming said normalized data set $\{NC_m(k)\}$ to obtain a transformed data set $\{TC_m(k)\}$, where said transformed data set $\{TC_m(k)\}$ is said second data set of said processed reference profile PC_m;

wherein said transforming is carried out for an experiment according to equations

$$TA_m(k) = f(x) = \frac{2n\left[\frac{b^2+2\cdot a^2\cdot NA_m(k)}{a} + 2\cdot\sqrt{a^2+b^2\cdot NA_m(k)+a^2\cdot[NA_m(k)]^2}\right]}{a} + d,$$

for $NA_m(k)>0$

and

$$TC_m(k) = f(x) = \frac{2n\left[\frac{b^2+2\cdot a^2\cdot NC_m(k)}{a} + 2\cdot\sqrt{a^2+b^2\cdot NC_m(k)+a^2\cdot[NC_m(k)]^2}\right]}{a} + d,$$

for $NC_m(k)>0$

where d is described by equation

$$d = \frac{2n\left[\frac{b^2}{a}+2\cdot a\right]}{a}$$

and where a is the fractional error coefficient of said experiment, b is the Poisson error coefficient of said experiment, and c is the standard deviation of background noise of said experiment.

165. (Canceled)

166. (Previously Presented) The computer system of claim 158, wherein said processing step (a) comprises:

normalizing each said experiment profile XA_m and reference profile XC_m to generate normalized data set $\{NA_m(k)\}$ and normalized data set $\{NC_m(k)\}$, respectively;

transforming said normalized data set $\{NA_m(k)\}$ to obtain a transformed data set $\{TA_m(k)\}$;

transforming said normalized data set $\{NC_m(k)\}$ to obtain a transformed data set $\{TC_m(k)\}$; and

removing nonlinearity from each said transformed data sets $\{TA_m(k)\}$ and $\{TC_m(k)\}$, respectively;

wherein said transforming is carried out for an experiment according to equations

$$TA_m(k) = f(x) = \frac{1}{a}\left[\frac{b^2+2\cdot a^2\cdot NA_m(k)}{4} - 2\cdot\sqrt{c^2+b^2\cdot NA_m(k)+a^2\cdot[NA_m(k)]^2}\right] + d,$$

for $NA_m(k)>0$

and

$$TC_m(k) = f(x) = \frac{\ln\left[\frac{b^2 + 2a - a^2 \cdot NC_m(k) + 2\sqrt{c^2 + b^2 \cdot NC_m(k) + a^2 \cdot [NC_m(k)]^2}}{b}\right]}{a} + d,$$

for $NC_m(k)>0$

where d is described by equation

$$d = \frac{-\ln\left[\frac{b^2}{c^2} + 2 - a\right]}{a}$$

and where a is the fractional error coefficient of said experiment, b is the Poisson error coefficient of said experiment, and c is the standard deviation of background noise of said experiment.

167. (**Currently Amended**) The computer system of claim 166, wherein said removing nonlinearity is carried out by a method comprising

(a1) calculating an average transformed profile of transformed experiment profiles and transformed reference profiles, wherein each of said transformed experiment profiles contains a corresponding ~~**error-model-based transformed or logarithm-based**~~ transformed data set $\{TA_m(k)\}$, and each of said transformed reference profiles contains a corresponding ~~**error-model-based transformed measurements or logarithm-based**~~ transformed data set $\{TC_m(k)\}$; and

(a2) calculating first differences between each of said transformed experiment profiles and said average transformed profile; calculating second differences between each of said transformed reference profiles and said average transformed profile; adjusting, wherein the adjusting comprises correcting nonlinearity each of said transformed experiment profiles based on said first

differences between each of said transformed experiment profiles and said average transformed profile, and adjusting, wherein the adjusting comprises correcting nonlinearity each of said transformed reference profiles based on said second differences between each of said transformed reference profiles and said average transformed profile.

168. (Previously Presented) The computer system of claim 167, wherein the method further comprises calculating said first differences based on the differences in a first subset of ~~error model based transformed measurements, or logarithm based~~ transformed measurements of said plurality of different cellular constituents between each of said transformed experiment profiles and said average transformed profile, and calculating said second differences based on the differences in a second subset of ~~error model based transformed measurements, or logarithm based~~ transformed measurements of said plurality of different cellular constituents between each of said transformed reference profiles and said average transformed profile.

169. (Previously Presented) The computer system of claim 168, wherein each said first subset consists of transformed measurements that are ranked similarly between each of said transformed experiment profiles and said average transformed profile, and each said second subset consists of transformed measurements that are ranked similarly between each of said transformed reference profiles and said average transformed profile.

170. (**Currently Amended**) The computer system of claim 169, wherein said adjusting step (a2) is carried out by a method comprising:

(a2i) binning said first subset into a plurality of bins, each said bin consisting of ~~error-model-based transformed~~ **measurements or logarithm-based** transformed measurements of said plurality of different cellular constituents in one of said transformed experiment profiles and said average transformed profile having a value in a given range; and binning said second subset into a plurality of bins, each said bin consisting of ~~error-model-based transformed measurements or logarithm-based~~ transformed measurements of said plurality of different cellular constituents in one of said transformed reference profiles and said average transformed profile having a value in a given range;

(a2ii) calculating, in each bin of said plurality of bins, a first mean difference between a feature value of ~~error-model-based transformed measurements or logarithm-based~~ transformed measurements of said plurality of different cellular constituents in said one of said transformed experiment profiles and a feature value of said average transformed profile, and calculating a second mean difference between a feature value of ~~error-model-based transformed measurements or logarithm-based~~ transformed measurements of said plurality of different cellular constituents in said one of said reference profiles and a feature value of the average profile;

(a2iii) determining a first curve of said first mean difference as a first function of values of ~~error-model-based transformed measurements or logarithm-based~~ transformed measurements of said plurality of different cellular constituents for said one

of said transformed experiment profiles, wherein said first function is represented by, $nonlinear\_TA_m$ and determining a second curve of said second mean difference as a second function of values of ~~error-model-based transformed measurements or logarithm-based~~ transformed measurements of said plurality of different cellular constituents for said one of said transformed reference profiles, wherein said second function is represented by $nonlinear\_TC_m$; and

(a2iv) computing corrected ~~error-model-based transformed measurements or logarithm-based~~ transformed measurements of said plurality of different cellular constituents in each said transformed data set $\{TA_m(k)\}$, according to the equation:

$$TA_m^{corr}(k) = TA_m(k) - nonlinear\_TA_m(k),$$

and computing corrected ~~error-model-based transformed measurements or logarithm-based~~ transformed measurements of said plurality of different cellular constituents in each said transformed data set $\{TC_m(k)\}$, according to the equation:

$$TC_m^{corr}(k) = TC_m(k) - nonlinear\_TC_m(k),$$

where k = 1, ..., N; and where $\{TA_m^{corr}(k)\}$ is said first processed data set of said processed experiment profile PA_m, and $\{TC_m^{corr}(k)\}$ is said second processed data set of said processed reference profile PC_m.

171. (**Currently Amended**) The computer system of claim 170, wherein said processed experiment profile PA_m and said processed reference profile PC_m comprise ~~error-model-based transformed measurements or logarithm-based~~ transformed

measurements of said plurality of different cellular constituents from the same experimental reaction.

172. (**Currently Amended**) The computer system of claim 171, wherein the method further comprises calculating $\overline{PC}(k)$ according to the equation

$$\overline{PC}(k) = \frac{1}{M} \sum_{m=1}^{M} PC_m(k),$$

wherein $\{PC_m(k)\}$ comprises ~~error-model-based transformed measurements or logarithm-based~~ transformed measurements from said second processed data set $\{TC_m^{corr}(k)\}$ and calculating said differential reference profile according to the equation

$$PC_{diff}(m,k) = PC_m(k) - \overline{PC}(k)$$

and wherein said first error-corrected profile is calculated according to the equation

$$PA'_m(k) = PA_m(k) - PC_{diff}(m,k),$$

wherein $\{PA_m(k)\}$ comprises ~~error-model-based transformed measurements or logarithm-based~~ transformed measurements from said first data set $\{TA_m^{corr}(k)\}$.

173. (Previously Presented) The computer system of claim 172, wherein the method further comprises

(d) calculating for each processed profile pair $\{PA_m, PC_m\}$, where $m \in \{1, 2, \ldots M\}$, a second error-corrected experiment profile PA''_m comprising data set $\{PA''_m(k)\}$ by

combining said first error-corrected experiment profile PA'_m with said processed experiment profile PA_m using a weighing factor $\{w(k)\}$, k = 1,2, ..., N, wherein $w(k)$ is a weighing factor for the k'th measurement.

174. (Previously Presented) The computer system of claim 173, wherein said second error-corrected experiment profile PA''_m is calculated according to the equation

$$PA''_m(k) = (1-w(k)) \cdot PA_m(k) + w(k)PA'_m(k).$$

175. (Previously Presented) The computer system of claim 174, wherein the method further comprises determining said weighing factor according to the equation

$$w(k) = 1-e^{-0.5\left[\frac{\overline{PA}(k)}{avg\_bkgstd}\right]^2}$$

where *avg_bkgstd* is an average background standard error.

176. (Previously Presented) The computer system of claim 175, wherein the method further comprises determining said *avg_ bkgstd* according to the equation

$$avg\_bkgstd = \frac{1}{N}\sum_{k=1}^{N}\left[\frac{1}{M}\sum_{m=1}^{M} bkgstd(m,k)\right]$$

where *bkgstd (m, k)* is background standard error of $PC_m(k)$.

177. (Previously Presented) The computer system of claim 172, wherein the method further comprises determining errors $\{P\sigma'_m\}$ of said first error-corrected experiment profile $\{PA'_m\}$, wherein said $\{P\sigma'_m\}$ comprises error data set $\{P\sigma'_m(k)\}$.

178. (Previously Presented) The computer system of claim 177, wherein the method further comprises determining said error data set $\{P\sigma'_m(k)\}$ according to the equation

$$\sigma'_m(k) = \sqrt{P\sigma_m^2(k) - mixed\_P\sigma_m^2(k) - 2Cor(k) \cdot P\sigma_m(k) \cdot mixed\_P\sigma_m(k)}$$

where $P\sigma_m(k)$ is the standard error of $A_m(k)$, and determining $mixed\_P\sigma_m(k)$ according to the equation

$$mixed\_P\sigma_m(k) = \frac{P\sigma_m(k) + (M-1)\cdot P\sigma_{avg}(k)}{M}$$

where

$$P\sigma_{avg}(k) = \sqrt{\frac{1}{M-1}\sum_{m}^{M}(PC_m(k) - \overline{PC}(k))^2}$$

and where Cor(k) is a correlation coefficient between said processed experiment profile PA_m and said processed reference profile PC_m.

179. (Previously Presented) The computer system of claim 178, wherein said Cor(k) is determined according to the equation

$$Cor(k) = CorMax \cdot \left[1 - e^{-0.5\left[\frac{PC(k)}{\text{average PC(k)}}\right]^4}\right]$$

where CorMax is a number between 0 and 1.

180. (Previously Presented) The computer system of claim 179, wherein the

method further comprises determining errors $\{P\sigma''_m\}$ of said second error-corrected experiment profile $\{PA''_m\}$ wherein said $\{P\sigma''_m\}$ comprises error data set $\{P\sigma''_m(k)\}$.

181. (Previously Presented) The computer system of claim 180, wherein the method further comprises determining said error data set $\{P\sigma''_m(k)\}$ according to the equation

$$P\sigma''_m(k) = \sqrt{[1 - w(k)] \cdot P\sigma_m^2(k) + w(k)P\sigma'^2_m(k)}$$

where $P\sigma_m(k)$ is the standard error of $PA_m(k)$, and the method further comprises determining $P\sigma'_m(k)$ according to the equation

$$P\sigma'_m(k) = \sqrt{P\sigma_m^2(k) + mixed\_P\sigma_m^2(k) - 2 \cdot Cor(k) \cdot P\sigma_m(k) \cdot mixed\_P\sigma_m(k)},$$

and

the method further comprises determining $mixed\_P\sigma_m(k)$ according to the equation

$$mixed\_P\sigma_m(k) = \frac{P\sigma_m(k) + (M-1)P\sigma_{wgf}(k)}{M}$$

where

$$P\sigma_{wgf}(k) = \sqrt{\frac{1}{M-1}\sum_{m}^{M} (PC_m(k) - \overline{PC}(k))^2}$$

and where Cor(k) is a correlation coefficient between said processed experiment profile PA_m and said processed reference profile PC_m.

182. (Previously Presented) The computer system of claim 181, wherein the method further comprises determining said Cor(k) according to the equation

$$Cor(k) = CorMax \cdot \left[1 - e^{-0.5\left[\frac{\overline{XC_k}}{avg\_avgstd}\right]^2}\right]$$

where CorMax is a number between 0 and 1.

183. (Previously Presented) The computer system of claim 182, wherein each said pair of profiles XA_m and XC_m comprise measurements of said plurality of different cellular constituents from a two-channel microarray experiment.

184. (Previously Presented) The computer system of claim 183, wherein said reference profiles $\{XC_m\}$, m = 1, 2, ... , M, are measured with samples labeled with a same label.

185. (Previously Presented) The computer system of claim 184, wherein at least one of said pairs of profiles $\{XA_m, XC_m\}$ is a virtual profile.

186. (**Currently Amended**) A computer system comprising:

a processor; and

a memory coupled to said processor and encoding one or more programs;

wherein said one or more programs cause the processor to carry out a method for generating at least one error-corrected experiment profile of at least one

experiment profile A_m, where $m \in \{1, 2, ..., M\}$ in at least one of a plurality of pairs of profiles $\{A_m, C_m\}$, A_m being an experiment profile, C_m being a reference profile, where $m = 1, 2, ..., M$, M is the number of pairs of profiles, said method comprising:

via ~~said~~ a differential reference profile $\underline{C_{diff}(m,k)}$ calculated between C_m and an average reference profile $\bar{C}$ determined for profile pair $\{A_m, C_m\}$ where $m \in \{1, 2, ..., M\}$, **wherein said average reference profile $\bar{C}$ comprises data set $\{\bar{C}(k)\}$,**

removing, on a computer, systematic cross-experiment error from said experiment profile A_m to generate a first error-corrected experiment profile A'_m; wherein said average reference profile $\bar{C}$ is an average of reference profiles $\{C_m\}$, $m = 1, 2, ..., M$; wherein for each $m \in \{1, 2, ..., M\}$, said first error-corrected experiment profile A'_m comprises data set $\{A'_m(k)\}$, said experiment profile A_m comprises data set $\{A_m(k)\}$, **and** said reference profile C_m comprises data set $\{C_m(k)\}$, ~~**and said average reference profile $\bar{C}$ comprises data set $\{\bar{C}(k)\}$,**~~ wherein said data set $\{A_m(k)\}$ comprises measurements~~**, error-model-based transformed measurements, or logarithm-based transformed measurements**~~ of a plurality of different cellular constituents measured in a sample having been subject to a first condition, said data set $\{C_m(k)\}$ comprises measurements~~**, error-model-based transformed measurements, or logarithm-based transformed measurements**~~ of said plurality of different cellular constituents measured in a sample having been subject to a second condition, wherein $k = 1, 2, ..., N$; k is an index of measurements~~**, error-model-based transformed measurements, or logarithm-based transformed measurements**~~

of cellular constituents, N being the total number of measurements, **wherein said first error-corrected experiment profile A'_m is generated according to the equation $A'_m(k) = A_m(k) - C_{m,r}(m,k)$;**

~~**obtaining data set $\{A''_m(k)\}$, wherein obtaining said data set $\{A''_m(k)\}$ comprises combining said first error-corrected experiment profile A'_m with said experiment profile A_m using a weighing factor $\{w(k)\}$, k = 1, 2, ... , N, wherein $w(k)$ is a weighing factor for a k^{th} measurement;**~~ and

outputting to a user, a user interface device, a computer readable storage medium, or a local or remote computer system; or displaying: said first error-corrected experiment profile $A'_m[[,]]$ or said data set $\{A'_m(k)\}$ ~~**, a second error-corrected experiment profile A''_m, or said data set $\{A''_m(k)\}$, wherein said second error-corrected experiment profile A''_m comprises said data set $\{A''_m(k)\}$**~~.

187. (Previously Presented) The computer system of claim 147, wherein the method further comprises obtaining said error-model-based transformed measurements of said data set $\{A_m(k)\}$ and said data set $\{C_m(k)\}$ for an experiment according to the equations:

$$A_m(k) = f(x) = \frac{\ln\left[\frac{b^2 + 2 \cdot a^2 \cdot XA_m(k)}{a} + 2\sqrt{c^2 + b^2 \cdot XA_m(k) + a^2 \cdot [XA_m(k)]^2}\right]}{a} + d,$$

for $XA_m(k)>0$

and

$$C_m(k) = f(x) = \frac{\ln\left[\frac{x^2 + z \cdot a^2 \cdot XC_m(k)}{n} + 2\sqrt{a^2 \cdot b^2 \cdot zC_m(k) + a^2 \cdot [XC_m(k)]^2}\right]}{\alpha} + d,$$

for $XC_m(k)>0$

where $\{XA_m(k)\}$ and $\{XC_m(k)\}$ are data sets comprising measurements of said plurality of different cellular constituents that when transformed produce said error-model-based transformed measurements of said plurality of different cellular constituents of said data set $A_m(k)$ and said data set $C_m(k)$, respectively, where d is described by the equation:

$$d = \frac{-\ln\left[\frac{x^2}{\alpha} + 3 \cdot c\right]}{\alpha}$$

and where a is the fractional error coefficient of said experiment, b is the Poisson error coefficient of said experiment, and c is the standard deviation of background noise of said experiment.

188. (Previously Presented) The computer system of claim 158, wherein said processing comprises:

normalizing, transforming, and/or removing nonlinearity from measurements of said plurality of cellular constituents of said data set $\{XA_m(k)\}$ of said experiment profile XA_m, and from measurements of said plurality of cellular constituents of said data set $\{XC_m(k)\}$ of said reference profile XC_m.

The following is an examiner's statement of reasons for allowance:

No art shows a differential reference profile computed between reference profiles and an average reference profile, and producing an error-corrected experiment profile by subtracting the differential reference profile from experiment.

Any comments considered necessary by applicant must be submitted no later than the payment of the issue fee and, to avoid processing delays, should preferably accompany the issue fee. Such submissions should be clearly labeled "Comments on Statement of Reasons for Allowance."

Conclusion

Claims 1-18, 20-30, 32-36, 38-57, 66, 67, 70-105, 107-164 and 166-188 are allowed.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to LARRY D. RIGGS II whose telephone number is (571)270-3062. The examiner can normally be reached on Monday-Thursday, 7:30AM-5:00PM, ALT. Friday, EST.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Marjorie Moran can be reached on 571-272-0720. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

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